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29: em vi: *
30: em htg hum: *
31: em htg inv: *
32: em htg other: *
33: em htg mus: *
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37: em htg vrt: *
38: em sy: *
39: em atgo hum: *
40: em atgo mus: *
41: em atgo other: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
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2	148	48.8	3267	6	AX045719	AX045719 Sequence
3	148	48.8	3716	9	AX358083	AX358083 Homo sapi
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5	120	39.6	756	6	AX870164	AX870164 Sequence
6	120	39.6	756	6	BD150226	BD150226 Primer fo
7	120	39.6	4262	6	AX883179	AX883179 Sequence
8	120	39.6	4262	6	BD012213	BD012213 Novel Gen
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10	120	39.6	4262	6	AX027852	AX027852 Homo sapi
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13	69	22.8	4694	9	AX074163	AX074163 Homo sapi
14	40	13.2	232	6	BD204437	BD204437 5' EST and
15	27	8.9	2886	10	AY277635	AY277635 Rattus no
16	25	8.3	195712	2	AC105958	AC105958 Mus muscu
17	25	8.3	220266	10	AC138284	AC138284 Mus muscu
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19	25	8.3	250318	2	AC109983	AC109983 Rattus no
20	10	3.3	887	8	AK107743	AK107743 Oryza sat
21	10	3.3	1298	8	AK071342	AK071342 Oryza sat
22	10	3.3	1309	10	MMU319657	BJ319657 Mus muscu
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ALIGNMENTS

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame plus p2n model

Run on: February 29, 2004, 22:51:23 ; Search time 4429 Seconds
(without alignments)
2965.215 Million cell updates

Title: US-10-047-021-86
 Perfect score: 303
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Searched: 3470272 seqs, 21671516995 residues

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Word size: 1
Total number of hits satisfying chosen parameters: 6934743

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post-processing: Listing first 45 summaries

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BD074325
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DEFINITION 50 human secreted proteins.
ACCESSION BD074325
VERSION BD074325.1 GI:22619928
KEYWORDS JP 2001514024-A/30.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1346)
AUTHORS Moore,P.A., Ruben,S.M., Lafleur,D.W., Shi,Y., Rosen,C.A.,
Olsen,H.S., Ebner,R. and Brewer,L.A.
TITLE 50 human secreted proteins
JOURNAL Patent: JP 2001514024-A 30 11-SEP-2001;
HUMAN GENOME SCIENCES INC
COMMENT OS Homo sapiens (human)
PN JP 2001514024-A/30
PD 11-SEP-2001
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PR 05-SEP-1997 US 60/057626,05-SEP-1997 US 60/057663 PR
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12-SEP-1997 US 60/058974,12-SEP-1997 US 60/058973 PR
12-SEP-1997 US 60/058666
PI PAUL A MOORE, STEVEN M RUBEN, DAVID W LAFLEUR, YANGLU SHI, CRAIG A
ROSEN,
PI HENRIK S OLSEN, REINHARD EBNER, LAURIE A BREWER PC
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FT Location/Qualifiers
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QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
DB 151 CAGTGTGTCCAGGGCCCTGGGCCCTCCAGGATGAGTCCGAGCTCAGGCCAGCCACCT 210
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LOCUS Sequence 134 from Patent WO0222660.
ACCESSION AX405719
VERSION AX405719.1 GI:21438877
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Tang,Y.T., Liu,C., Zhou,P., Asundi,V., Zhang,J., Zhao,Q.A., Ren,F.,
Xue,A.J., Yang,Y., Wehrman,T. and Drmanac,R.T.
TITLE Novel nucleic acids and polypeptides
JOURNAL Patent: WO 0222660-A 134 21-MAR-2002;
HYSEQ, INC. (US)
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REFERENCE 1 (bases 1 to 3716)
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Clark,H.F., Chui,C., Crowley,C., Grimaldi,C., Gu,Q., Hass,P.E.,
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Stinson,J., Vagts,A., Vanden.R., Watanabe,C., Wiedon,D., Woods,K.,
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2285-2270 (2003)
REFERENCE 2 (bases 1 to 3716)
AUTHORS Clark,H.F.
DIRECT SUBMISSION
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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CDS

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PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAYATSU,
PI KENICHI NAGAI, TETSUJI OTSUKI
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QY 100 sAspGlyGlnAlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLe 120
DB 339 CGATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGCT 398
QY 120 uGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGl 140
DB 399 TGGCAGCGCAGCTCAGACAGAGCGTGGCTGTCTGTGCTGTCTCCCGGAGGATTTCCA 458
QY 140 nIleGlnProArgAspMetValAlaValValGlyGlnPheThrLeuGluCysGlyPr 160
DB 459 GATCCAGCCTCGACACATGCTGGCTGTGTGGTGGGTAGCAGTTTACTCTGGATGTGGGCC 518
QY 160 oProTrpGlyHisProGluProThrValSerTrpTrpLysAspGly-LysProLeuAlaL 180
DB 519 GCCCTGGGGCCACCCAGAGCCACAGTCTCATGTGTGGAAGATCA-GAAACCCCTGGCCC 577
QY 180 euGlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLys 200
DB 578 TCCAGCCCGAAGGCACACATGTTCGGGGGGGTCCCTGCTGATGGCAGAGCAGAGAGA 637

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QY 200 erAspGlu 202
DB 638 GTGACGAA 645

RESULT 7
LOCUS AX883179 4262 bp DNA linear PAT 17-DEC-2003
DEFINITION Sequence 18084 from Patent EP1074617.
ACCESSION AX883179
VERSION AX883179.1 GI:40038080
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
TITLE Primers for synthesizing full-length cDNA and their use
JOURNAL Patent: EP 1074617-A 18084 07-FEB-2001;
Research Association for Biotechnology (JRP)
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ORIGIN

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Alignment Scores:
Pred. No.: 2, 65e-108 Length: 4262
Score: 120.00 Matches: 263
Percent Similarity: 97.77% Conservative: 0
Best Local Similarity: 97.77% Mismatches: 3
Query Match: 39.60% Indels: 6
DB: 6 Gaps: 0

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QY 21 LeuLeuMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp 40
DB 100 CTCATCATGGGAGGAGCATGGCTCAGGACTCCCGGCCCGCCAGATCTAGTCCACCCCGAGGAC 159
QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProPr 60
DB 160 CAGCTGTCTCCAGGGCCCTGGCCCTGCCAGGTAGCTGCCA-AGCCTCAGGCGAGCCACC 218
QY 60 oProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHi 80
DB 219 TCCCAACCATCCGCTGGTGTGCTGAATGGGCGAGCCCTGAGCATGTGCTCCCGCCAGACCCACA 278

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PI JUNICHI NEZU
PC C12N15/54, C12N15/55, C12N9/12, C12N9/16, C12N5/10, C12N1/21 PC
, C12N1/19, C07K16/40,
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Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.: 2,65e-108 Length: 4262
Score: 120.00 Matches: 263
Percent Similarity: 97.77% Conservative: 0
Best Local Similarity: 97.77% Mismatches: 3
Query Match: 39.60% Indels: 6
DB: Gaps: 0

US-10-047-021-86 (1-303) x BD012213 (1-4262)

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QY 21 LeuLeuMetGlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAsp 40
DB 100 CTCATCATGGGAGGAGCTGCTCAGACTCCCGGCCAGATCTCTAGTCAACCCCGAGAC 159
QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProPr 60
DB 160 CAGCTGTTCAGGGCCCTGGCCCTCCAGGATGAGTGCCTCA-AGCCTCAGGCCACCCACC 218
QY 60 oProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHi 80
DB 219 TCCACCACTCCGCTGGTGTCTGAATGGGAGCCCTGAGCATGGTCCGCCAGACCCACA 278
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DB 279 CCACCTCCGCTGATGGGAGCCCTTCTGCTGTACAGCCCTGCCGGGACATGCCCA 338
QY 100 sAspGlyGlnAlaLeuSerThrAspLeuGlyValTrpThrCysGluAlaSerAsnArgLe 120
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QY 120 uGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGl 140
DB 399 TGGCAGCGGAGTCCAGCAGAGCGCTCGGCTGTCTGTGGCTGTCTCCGGGAGGATTTCCA 458
QY 140 nileGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPr 160
DB 459 GATCAGCCCTCGAGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCC 518
QY 160 oProTrpGlyHisProGluProThrValSerTrpTrpLysAspGly-LysProLeuAlaL 180
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QY 180 euGlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysS 200
DB 578 TCAGCCCCGGAAGGCACACAGTGTCCGGGGGTCTCTGCTGTATGGCAAGAGCAGAGAGA 637
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DB 638 GTGACGAAGG-GACCTTACATGTGTGGGCCACCAACAGCGCAGGACACAGGAGAGCCGC 696
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QY 240 ValArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLys 259

QY 80 shisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHi 100
DB 279 CCACCTCTGCTGATGGGAGCTTCTGTGCTACAGCCCTGTCCGGGAGCATGCCCA 338
QY 100 sAspGlyGlnAlaLeuSerThrAspLeuGlyValTrpThrCysGluAlaSerAsnArgLe 120
DB 339 CGATGGCCAGGCCCTGTCCACAGCTGGTGTCTACACATGTGAGGCCAGCAACCGGCT 398
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QY 160 oProTrpGlyHisProGluProThrValSerTrpTrpLysAspGly-LysProLeuAlaL 180
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QY 180 euGlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysS 200
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QY 260 ProArgProAlaValTrpLeu 266
DB 817 CCTAGACGGCGGTGTGGCTC 837

RESULT 8
BD012213
LOCUS
DEFINITION Novel genes encoding protein kinase or protein phosphatase.
ACCESSION BD012213
VERSION BD012213.1 GI:22092402
KEYWORDS WO 0109345-A/11.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4262)
Ota,I., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K., Otsuki,T.,
Funahashi,S., Sano,C. and Nezu,J.
Novel genes encoding protein kinase or protein phosphatase
Patent: WO 0109345-A 11 08-FEB-2001;
HELIX RESEARCH INSTITUTE, TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA,
KOJI HAYASHI, KAORU SAITO, JUNICHI YAMAMOTO, SHIZUKO ISHII, OMOYASU
SUGIYAMA, AI WAKAMATSU, KEIICHI NAGAI, TETSUJI OTSUKI, SHINICHI
FUNAHASHI, HIAKI SENO, JUNICHI NEZU
OS Homo sapiens (human)
PN WO 0109345-A/11
PD 08-FEB-2001
PF 28-JUL-2000 WO 2000JP005060
PR 29-JUL-1999 JP 99P 248036, 11-JAN-2000 JP 00P 118776 PR
02-MAY-2000 JP 00P 183767, 18-OCT-1999 US 60/159590 PR
17-FEB-2000 US 60/183322
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, PI
KAORU SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI, SHINICHI FUNAHASHI, CHIYAKI SENO,
PI

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Db      757 GTGCCAAATTCAGCTGGAAAAATGTGACACTGTGTAACCCGCGATCTCTGCAGAGGCGCCCAAG 816
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LOCUS   BD160172
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD160172
VERSION   BD160172.1 GI:27865930
KEYWORDS JP 2002191363-A/15015.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
TITLE   Primer for synthesizing full-length cDNA and use thereof
JOURNAL HELIX RESEARCH INSTITUTE
COMMENT  Patent: JP 2002191363-A 15015 09-JUL-2002;
        OS Homo sapiens (human)
        PN JP 2002191363-A/15015
        PD 09-JUL-2002
        PF 28-JUL-2000 JP 2000280990
        PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU SAITO, JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU, PI KEIICHI NAGAI, TETSUJI OTSUKI
        PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
        PC Primer for synthesizing full-length cDNA and use thereof PH Key
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Alignment Scores:
Pred. No.: 2,65e-108 Length: 4262
Score: 120.00 Matches: 263
Percent Similarity: 97.77% Conservative: 0
Best Local Similarity: 97.77% Mismatches: 3
Query Match: 39.60% Indels: 6
DB: 6 Gaps: 0

US-10-047-021-86 (1-303) x BD160172 (1-4262)

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Db      100 CTCATCATGGAGGAGCATGGCTCAGAGACTCCCGCGCCAGATCTTAGTCCACCCCGAGGAC 159
QY      41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProPr 60
Db      160 CAGCTGTTCACAGGGCCCTGGCCCTGCCAGATGAGCTGCCA-AGCCTCAGCGCCAGCCACC 218
QY      60 oProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHi 80
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Db      279 CCACCTTCCTGCCTGATGGGACCCCTTCTGTGTACAGCCCCCTGCCGGGGACATGCCCA 338
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Db      339 CGATGGCCAGGCGCTGTCCACAGACCTGGGTCTTACACATGTGAGGCAGCACACCGGCT 398
QY      120 uGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheG1 140
Db      399 TGGCAGCGGAGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCTCCGGAGGATTTCCA 458
QY      140 nIleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPr 160
Db      459 GATCCAGCCCTCGAGACATGTGTGTGTGGTGGTGGAGTCTTACTCTGGAATGTGGGCC 518
QY      160 oProTrpGlyHisProGluProThrValSerTrpTrpIysAspGly-LysProLeuAlaL 180
Db      519 GGCCTGGGGCCACCCAGAGCCACAGTCTCATGTGGTGGAAAGATGA-GAAACCCCTGGGCC 577
QY      180 euGlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLys 200
Db      578 TCCAGCCCGAAGGACACACAGTGTCCGGGGGTCTCTGTGTGATGGCAAGACGAGAGA 637
QY      200 erAspGlu***-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArg 219
Db      638 GTGACGAGAGG-GACCTTACATGTGTGTGGCCACCAACAGCGCAGGACACAGGAGAGCGCC 696
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QY      240 ValArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLys 259
Db      757 GTGCGAATTCAGCTGGAAAAATGTGACACTGTCTGAACCCCGGATCTCTGCAGAGGCGCCCAAG 816
QY      260 ProArgProAlaValTriPleu 266
Db      817 CCTAGACCGCGCGTGTGGCTC 837

RESULT 10
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LOCUS   Homo sapiens cDNA FLJ14946 f1s, clone PLACE2000034, weakly similar
DEFINITION to LAR PROTEIN PRECURSOR (EC 3.1.1.3.48).
ACCESSION AK027852
VERSION   AK027852.1 GI:14042831
KEYWORDS oligo capping; f1s (full insert sequence).
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Nabekura, T., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagehara, K., Masuho, Y. and Oshima, A.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 4262)
Isogai, T. and Otsuki, T.
Direct Submission
Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: 5'- & 3'- end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
TITLE   JOURNAL
REFERENCE
AUTHORS Isogai, T. and Otsuki, T.
TITLE   Direct Submission
JOURNAL Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: 5'- & 3'- end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

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	CSRRLSPSLSLAPAAWAKKQELPHANSPLLRGSHSLLELRACELGNRSKNLS				
	QSPGAVPQALVAMRALGPKLLSSOMSLVLSLQHPSLFKMLPQLRVNRPRLRHRL				
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ORIGIN					
Alignment Scores:					
Pred. No.:	2,65e-108	Length:	4262		
Score:	120.00	Matches:	263		
Percent Similarity:	97.77%	Conservative:	0		
Best Local Similarity:	97.77%	Mismatches:	3		
Query Match:	39.60%	Indels:	6		
DB:	9	Gaps:	0		
US-10-047-021-86 (1-303) x AK027852 (1-4262)					
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Db	40	ATGGGCTCTGGAGGACAGAGCTCTGGGGGAGAGGGTTCCTGCTGCTGCTGCTG 99			
Qy	21	LeuLeuMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp 40			
Db	100	CTCATCATGGAGGACATGGCTCAGGACTCCCGGCCCATGCTAGTCCATCCAGCCAGGAC 159			
Qy	41	GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProPr 60			
Db	160	CAGCTGTTCAGGGCCCTGGCCCTGCCAGATGAGTCCCA-AGCCTCAGGCCAGCCACC 218			
Qy	60	oProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValP-oProAspPrChi 80			
Db	219	TCCACCATCCGCTGTTGCTGAATGGCAGGCCCTGTAGCATGTGTGCCCCAGACCCACA 278			
Qy	80	sHisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHi 100			
Db	279	CCACCTCTGCTGTATGGAGCCCTTCTGCTGCTACAGCCCTCGCCGGGAGCATGGCCA 338			
Qy	100	sAspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLe 120			
Db	339	CGATGGCCAGGCCCTGTCTCAGACACCTGGGTGTCTACACATGTGAGGCACCAACCGGCT 398			
Qy	120	uGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGl 140			
Db	399	TGGCAGCGCAGTCCAGCAGAGCGCTCGGCTGTCTGTGCTGTCTCCGGAGGATTCCA 458			
Qy	140	nIleGlnProArgAspMetValAlaValValGlyGlnPheThrLeuGluCysGlyPr 160			
Db	459	GATCCAGCCTCGAGACATGGTGGCTGTGTGGGTGAGCAGTTTACTCTGGAATGTGGGCC 518			
Qy	160	oProTrpGlyHisProGluProThrValSerTrpTrpLysAspGly-LysProLeuAlaL 180			

Db	519	GCCTGGGGCCACCAGGAGCCACAGTCTCATGGTGAAGATGA-GAAACCCCTGGCCC 577
Qy	180	euGlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLys 200
Db	578	TCCAGCCCGGAGGACACACAGTCTCGGGGGTCCCTGCTGATGGCAAGAGCAGAGA 637
Qy	200	erAspGlu***-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArg 219
Db	638	GTGACGAGG-GACCTACATGTGTGTGGCCACCAACAGCGCAGGACACAGGAGGCCGC 696
Qy	220	AlaAlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAla 239
Db	697	GCAGCCCGGGTTTCCATCCAGGAGGCCACGAGCTACACGAGCCTGTGTGAGCTTTGGGT 756
Qy	240	ValArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLys 259
Db	757	GTGCGAATTCAGCTGGAAATGTGACACTGCTGAACCCGGAATCTTGCAGAGGCCCCCAAG 816
Qy	260	ProArgProAlaValTrpLeu 266
Db	817	CCTAGACGGCGGTGTGGCTC 837
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BC014995		
BC014995.1	GI:21955407	
Homo sapiens (human)		
Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
1 (bases 1 to 3467)		
Strausberg, R.		
Direct Submission		
Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
NIH-MGC Project URL: http://mgc.nci.nih.gov		
Contact: MGC help desk		
Email: cgapbs-remail.nih.gov		
Tissue Procurement: Dr. Mark Watson		
CDNA Library Preparation: Rubin Laboratory		
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)		
DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada		
info@bcgsc.bc.ca		
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McEavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schain, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Scott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.		
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov		
Series: IRAL Plate: 34 Row: a Column: 19		
Location/Qualifiers		
1. 3467		
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/lab_host="DH10B-R"		
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source		
FEATURES		
ORIGIN		

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 34 Row: a Column: 19.
Location/Qualifiers
1. 3467
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Alignment Scores:
 Pred. No.: 2,186-107 Length: 3467
 Score: 119.00 Matches: 182
 Percent Similarity: 98.91% Conservatives: 0
 Best Local Similarity: 98.91% Mismatches: 1
 Query Match: 39.27% Indels: 2
 DB: 9 Gaps: 0

US-10-047-021-86 (1-303) x BC014995 (1-3467)

QY 84 ProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyCln 103
 DB 2 CCGATGGGACCCCTTCTGCTACAGCCCTGCGCGGACATGCCACGATGGCCAG 61
 QY 104 AlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAla 123
 DB 62 GCCCTGTCCACAGACCTGGGTCTTACATGTGAGGCCACGACCGCTTGGCAGGCA 121
 QY 124 ValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPro 143
 DB 122 GTCCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCTTCCGGGAGGATTTCCAGATCCAGCCT 181
 QY 144 ArgAspMetValAlaValGlyGluGlnPheThrLeuGluCysGlyProProTyrGly 163
 DB 182 CGGGACATGGTGGCTGTGGTGGTGAGCAGTTACTCTGGATGTGGCCCGCCCTGGGGC 241
 QY 164 HisProGluProThrValSerTyrTrpLysAspGlyLysProLeuAlaLeuGlnProGly 183
 DB 242 CACCCAGAGCCACAGTCTCATGTGTGAAGATGGAAACCCCTGGCCCTCCAGCCCGGA 301
 QY 184 ArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu*** 203
 DB 302 AGGCACAGTGTCCGGGGGATCCCTGTGTATGGCAAGAGAGAGAGATGATGAGAGG- 360
 QY 204 -ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgVa 223
 DB 361 GACCTACATGTGTGGCCACCAACAGCGCAGGACACAGGAGAGCCGCGCGCGGT 420
 QY 223 LserIleGlnProGlnAspTyrThrGluProValGluLeuAlaValArgIleG1 243
 DB 421 TTCCATCCAGAGGCCACAGGACTACAGGAGCCTGTGGAGTCTTGTGCTGTGCGAATCA 480
 QY 243 nLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProAspProAl 263
 DB 481 GCTGGAAATGTGACATGCTGACCCCGGATCTTGCAGAGGCCCCAAGACCTAGACCGGC 540
 QY 263 aValTrpLeu 266
 DB 541 GGTGTGGCTC 550

RESULT 12
 AP003501/1
 LOCUS AP003501 186971 bp DNA linear PRI 08-MAR-2002
 DEFINITION Homo sapiens genomic DNA, chromosome 11q, clone:RP11-664121,
 complete sequence.
 ACCESSION AP003501
 VERSION AP003501.2 GI:19263048
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
 TITLE Homo sapiens genomic DNA
 JOURNAL Published Only in Database (2001)
 REFERENCE
 AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
 TITLE Homo sapiens genomic DNA
 JOURNAL Published Only in Database (2001)

1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
 Tel:81-45-503-9111, Fax:81-45-503-9170)
 On Mar 7, 2002 this sequence version replaced gi:13603460.

COMMENT
 FEATURES
 source

Location/Qualifiers
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 /mol_type="genomic DNA"
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ORIGIN

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 Percent Similarity: 98.20% Conservatives: 0
 Best Local Similarity: 98.20% Mismatches: 1
 Query Match: 26.07% Indels: 2
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US-10-047-021-86 (1-303) x AP003501 (1-186971)

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 DB 32342 GAGAGGATGGCTCAGACCTCCCGCCCGCAGATCTTAGTCCACCCGAGCAGCAGTGTTC 32283
 QY 44 GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProProThr11 63
 DB 32282 CAGGGCCCTGGCCCTGCCAGGATGAGTGCCA-AGCCTCAGGCCAGCACCTCCACCAT 32224
 QY 63 eArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLe 83
 DB 32223 CCGCTGTGTCTCAATGGCAGCCCTGAGCATGTGTGGTGGCCCGCAGACCCACACCTCCT 32164
 QY 83 uProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyG1 103
 DB 32163 GCCTGATGGAGCCCTTCTCTCTACAGCCCTCTCCCGGGGACATGCCAGATGGCCA 32104
 QY 103 nAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAl 123
 DB 32103 GGCCTGTGTCCACAGACCTGGGTGTCTACATGTGAGGCCAGCACCCGCTTGGCAGCGC 32044
 QY 123 aValSerArgGlyAlaArgLeuSerValAla 133
 DB 32043 AGTCAGCAGAGCGCTCGGCTGTCTGTGGCT 32013

RESULT 13

AK074163
 LOCUS AK074163 4694 bp mRNA linear PRI 15-FEB-2002
 DEFINITION Homo sapiens mRNA for FLJ00236 protein.
 ACCESSION AK074163
 VERSION AK074163.1 GI:18676673
 KEYWORDS fis (full insert sequence).
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS Jikuya,H., Takano,J., Nomura,N., Kikuno,R., Nagase,T. and Ohara,O.
 TITLE The nucleotide sequence of a long cDNA clone isolated from human spleen
 JOURNAL Published Only in Database (2002)
 REFERENCE
 AUTHORS Jikuya,H., Takano,J., Nomura,N., Kikuno,R., Nagase,T. and Ohara,O.
 TITLE Direct Submission
 JOURNAL Submitted (21-JAN-2002) Takahiro Nagase, Kazusa DNA Research
 Institute, Department of Human Gene Research; 1532-3, Yana,
 Kisarazu, Chiba 292-0812, Japan (E-mail:cdmainfo@kazusa.or.jp,
 URL:http://www.kazusa.or.jp/NEDO, Tel:81-438-52-3913,
 Fax:81-438-52-3914)

COMMENT
 NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert and 5'- & 3'-end one pass sequencing; Research Association for Biotechnology; cDNA library construction and clone selection; Kazusa DNA Research Institute.

FEATURES

Location/Qualifiers

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/clone="FLJ00236"
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1. 4694
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1. 2109
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SGPAAPQSYTALFRTQTGPGGAPWAEELAGWQSAELGHLHWGQDYEFKVRPSGG
RARGPNDLILRLPEKVPAPQEVTKFCNGTVFVSWVPPFAENHNGIIRGYQVMS
LGNTSLPANNVTVEGTQLEIAIHPGSCYCVAAVTGAGAGEPRPVCLLLEQAME
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SLLSWDRSPVLPDTSITFYGLIAELFSSITPAREPQVPAVRLLPPLQALSLSPC
SSDSLSRGLSFRSLPAEAWKAKKQELQHNSSPLDLSDHSLERACELGNR
GSKNLSQPGVAPLAWRALGPKLSSNLEIHLRPLPAPLFPHEHTPTQSQQTP
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LTPEVALCLELSSEGTTPR"

Gene

CDS

ORIGIN

Alignment Scores:

Pred. No.: 9.4e-58 Length: 4694
Score: 69.00 Matches: 132
Percent Similarity: 98.51% Conservative: 0
Best Local Similarity: 98.51% Mismatches: 1
Query Match: 22.77% Indels: 2
DB: 9 Gaps: 0

US-10-047-021-86 (1-303) x AK074163 (1-4694)

Qy 134 ValLeuArgGluAspPheGlnIleGlnProArgAspMetValAlaValValGlyGluGln 153
Db 70 GTCTCCGGAGGATTCCAGATCCAGCTCGGACATGGTGGCTGTGGTGGTGAGCAG 129
Qy 154 PheThrLeuGluCysGlyProProTrpGlyHisProGluProThrValSerTyrTrpIys 173
Db 130 TTACTCTGGAATGTGGGCGCCCTCGGCGCCACCCAGAGCCACAGTCTCATGTGGTGA 189
Qy 174 AspGlyLysProLeuAlaGlnProGlyArgHisThrValSerGlyGlySerLeuLeu 193
Db 190 GATGGGAACCCCTGGCCCTCAGCCCGAGAGGACACAGTGTCCGGGGGGTCTCTGCTG 249
Qy 194 MetAlaArgAlaGluLysSerAspGlu*** ThrTyrMetCysValAlaIleThrAsnSerAl 213
Db 250 ATGGCAAGACAGACAGAGTACCAAGG-CACCTACATGTGTGTGGCCACCAACAGCGC 308
Qy 213 aGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGluProGlnAspTyrThrG1 233
Db 309 AGGACATAGGAGAGCCCGAGCCCGGGTTTCCATCCAGAGCCCCAGGACTACACGGA 368
Qy 233 pProValGluLeuLeuAlaValArgIleGlnLeuGluAsnValThrLeuLeuAsnProAs 253
Db 369 GCCTGTGGAGCTTCTGGCTGTGGCAATTCAGCTGGAAAATGTGACACTGCTGAACCGGA 428
Qy 253 pProAlaGluGlyProLysProArgProAlaValTrpLeu 266

Db 429 TCCTGACGAGGGCCCCAAGACCTAGACCGCGGTGTGCTC 468

RESULT 14

BD204437 232 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION
5'EST and human protein encoded thereby.
ACCESSION
BD204437
VERSION
BD204437.1 GI:33014207
KEYWORDS
JP 2002511259-A/641.
SOURCE
Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS
Edwards,J.B.D.M., Duclert,A. and Giordano,J.Y.
TITLE
5'EST and human protein encoded thereby
JOURNAL
Patent: JP 2002511259-A 641 16-APR-2002;
GENSET

COMMENT

OS Homo sapiens (human)
PN JP 2002511259-A/641
PD 16-APR-2002
PF 09-APR-1999 JP 2000543599
PR 09-APR-1998 US 09/057719,28-APR-1998 US 09/069047 PI
JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCLERT,JEAN YVES PI
GIORDANO
PC C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12M1/00,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,C12P21/02,C12Q1/68,G01N33/53,G01N33/566, PC
G06F17/50//
PC G06F17/30,C12N15/00,C12N5/00,C12N15/00
CC Von Heijne matrix
CC score 3.7999995231628
CC seq JFLLPFAHGRHG/SG
CC Location/Qualifiers
FH Key
FT CDS
FT sig_peptide 41..232
FT Location/Qualifiers
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FEATURES

source

ORIGIN

Alignment Scores:
Pred. No.: 3.88e-30 Length: 232
Score: 40.00 Matches: 53
Percent Similarity: 98.15% Conservative: 0
Best Local Similarity: 98.15% Mismatches: 0
Query Match: 13.20% Indels: 1
DB: 6 Gaps: 0

US-10-047-021-86 (1-303) x BD204437 (1-232)

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Db 41 ATGGGCTCTGGAGGAGACACCTCTCTGGGGGCGAGGGGTTCCTGCTGTGCTCCCT 100
Qy 20 uLeuIleMetGlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAs 40
Db 101 GCTCATCATGGGAGGAGATGGCTCAGACTCCCGCCGCCAGATCCTAGTCCACCCCGGA 160
Qy 40 pGlnLeuPheGlnGlyProGlyProAlaArgMetSerCys 53
Db 161 CCAGCTGTTCCAGGGCCCTGGCCCTCCAGGATGAGCTGC 200

RESULT 15

AY277635 2886 bp mRNA linear ROD 12-MAY-2003
LOCUS
DEFINITION
Rattus norvegicus ROBO4 (Robo4) mRNA, complete cds.
ACCESSION
AY277635
VERSION
AY277635.1 GI:30575794
KEYWORDS

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 29, 2004, 08:17:17 ; Search time 52 Seconds

(without alignments)
1230.374 Million cell updates/sec

Title: US-10-047-021-86

Perfect score: 303

Sequence: 1 MGSGGSLGGRGSLPLLL.....SGPRLPREARELGRQRRNTG 303

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 809742 seqs, 21153259 residues

Word size : 0

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	300	99.0	304	14	US-10-411-224-86
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5	148	48.8	985	9	US-09-978-697-211
6	148	48.8	985	9	US-09-978-192A-211
7	148	48.8	985	9	US-09-999-832A-211
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9	148	48.8	985	10	US-09-978-608A-211
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11	148	48.8	985	10	US-09-978-191A-211
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37	148	48.8	985	14	US-10-013-929A-211
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44	148	48.8	985	14	US-10-145-128A-211
45	148	48.8	985	14	US-10-017-191A-211

ALIGNMENTS

RESULT 1

- US-10-047-021-86
- Sequence 86, Application US/10047021
- Publication No. US20040002591A1
- GENERAL INFORMATION:
- APPLICANT: Rosen et al.
- FILE REFERENCE: P2016P2
- CURRENT APPLICATION NUMBER: US/10/047,021
- PRIOR FILING DATE: 2002-01-15
- PRIOR APPLICATION NUMBER: US 60/262,066
- PRIOR FILING DATE: 2001-01-18
- PRIOR APPLICATION NUMBER: US 09/722,329
- PRIOR FILING DATE: 2000-11-28
- PRIOR APPLICATION NUMBER: US 09/262,109
- PRIOR FILING DATE: 1999-03-04
- PRIOR APPLICATION NUMBER: PCT/US98/18360
- PRIOR FILING DATE: 1998-09-03
- PRIOR APPLICATION NUMBER: US 60/057,626
- PRIOR FILING DATE: 1997-09-05
- PRIOR APPLICATION NUMBER: US 60/057,663
- PRIOR FILING DATE: 1997-09-05
- PRIOR APPLICATION NUMBER: US 60/057,669
- PRIOR FILING DATE: 1997-09-05
- PRIOR APPLICATION NUMBER: US 60/058,667
- PRIOR FILING DATE: 1997-09-12
- PRIOR APPLICATION NUMBER: US 60/058,974
- PRIOR FILING DATE: 1997-09-12
- PRIOR APPLICATION NUMBER: US 60/058,973
- PRIOR FILING DATE: 1997-09-12
- PRIOR APPLICATION NUMBER: US 60/058,666
- PRIOR FILING DATE: 1997-09-12
- PRIOR APPLICATION NUMBER: US 60/090,112
- PRIOR FILING DATE: 1998-06-22
- NUMBER OF SEQ ID NOS: 206
- SOFTWARE: PatentIn Ver. 2.0
- SEQ ID NO 86
- LENGTH: 303

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; ORGANISM: Homo sapiens
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; LOCATION: (203)
; OTHER INFORMATION: Xaa equals any amino acid
; NAME/KEY: SITE
; LOCATION: (267)
; OTHER INFORMATION: Xaa equals any amino acid
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; LOCATION: (274)
; OTHER INFORMATION: Xaa equals any amino acid
US-10-047-021-86

Query Match          99.0%; Score 300; DB 15; Length 303;
Best Local Similarity 100.0%; Pred. No. 3.9e-262;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 GTAVSRGARLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWKDGKPLAL 180
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QY 181 QPGRHTVSGSLLMARAESDXTTMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV 240
Db 181 QPGRHTVSGSLLMARAESDXTTMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV 240
QY 241 RIQLENVTLNPDPAEGPKPRPAVWLXWKVSGPXRLPNLTRPCSGPRLPREARELRGQR 300
Db 241 RIQLENVTLNPDPAEGPKPRPAVWLXWKVSGPXRLPNLTRPCSGPRLPREARELRGQR 300
QY 301 NTG 303
Db 301 NTG 303

RESULT 2
US-10-047-021-86
; Sequence 86, Application US/10411224
; Publication No. US20030166906A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 50 Human Secreted Proteins
; FILE REFERENCE: PZ016P1
; CURRENT APPLICATION NUMBER: US/10/411,224
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/09/722,329
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/262,109
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 60/057,626
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/057,663
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/058,667
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,974
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,973
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,666
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: 1998-06-22

; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 86
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (203)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (267)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (274)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; OTHER INFORMATION: Xaa equals stop translation
US-10-041-224-86

Query Match          99.0%; Score 300; DB 14; Length 304;
Best Local Similarity 100.0%; Pred. No. 3.9e-262;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGGDSLLGGRGSLPLLLLLIMGMAQDSPPQILVHPDQLFOGPGPARMSCRASGQPP 60
Db 1 MSGGDSLLGGRGSLPLLLLLIMGMAQDSPPQILVHPDQLFOGPGPARMSCRASGQPP 60
QY 61 PTIRLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAHQALSTDLGVYTCASNRL 120
Db 61 PTIRLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAHQALSTDLGVYTCASNRL 120
QY 121 GTAVSRGARLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWKDGKPLAL 180
Db 121 GTAVSRGARLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWKDGKPLAL 180
QY 181 QPGRHTVSGSLLMARAESDXTTMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV 240
Db 181 QPGRHTVSGSLLMARAESDXTTMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV 240
QY 241 RIQLENVTLNPDPAEGPKPRPAVWLXWKVSGPXRLPNLTRPCSGPRLPREARELRGQR 300
Db 241 RIQLENVTLNPDPAEGPKPRPAVWLXWKVSGPXRLPNLTRPCSGPRLPREARELRGQR 300
QY 301 NTG 303
Db 301 NTG 303

RESULT 3
US-09-796-753-158
; Sequence 158, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26

```

RESULT 4
US-09-978-295A-211
; Sequence 211, Application US/09978295A
; Patent No. US20020156008A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kijavini, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630P1C11
 CURRENT APPLICATION NUMBER: US/09/978,295A
 CURRENT FILING DATE: 2001-10-15
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/064249
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 48.8%; Score 148; DB 9; Length 985;

Best Local Similarity 100.0%; Pred. No. 1.1e-124;

Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 ASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGTTLLLOPPARGHADGQALSTDLGVYTC 114

Db 33 ASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGTTLLLOPPARGHADGQALSTDLGVYTC 92

QY 115 EASNRLGTAVSARGLSVAVLREDFQIOPRDNVAVVGQFTLECCPPNGHDEPTVSWMKD 174

Db 93 EASNRLGTAVSARGLSVAVLREDFQIOPRDNVAVVGQFTLECCPPNGHDEPTVSWMKD 152

QY 175 GKPLALQPCRHTVSGSLIMARAEXSDE 202

Db 153 GKPLALQPCRHTVSGSLIMARAEXSDE 180

RESULT 5:

US-09-978-697-211

; Sequence 211, Application US/09978697

; Patent No. US20020169284A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Fliviaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
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PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
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PRIOR APPLICATION NUMBER: 60/082797
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PRIOR FILING DATE: 1998-04-23
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PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
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; PRIOR FILING DATE: 1998-04-29
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 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 48.8%; Score 148; DB 9; Length 985;
 Best Local Similarity 100.0%; Pred. No. 1.1e-124;
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 55 ASGQPPPTIRWLNQPLSVPPDPHLLPDGTLILLQPPARGHAGDQALSTDLGVYTC 114
 Db 33 ASGQPPPTIRWLNQPLSVPPDPHLLPDGTLILLQPPARGHAGDQALSTDLGVYTC 92
 Qy 115 EASNRLGTAVSRGRLSVAVLRDEPQIQPRDMVAVVGEQFTLSCGPPWGHPEPTVSWKD 174
 Db 93 EASNRLGTAVSRGRLSVAVLRDEPQIQPRDMVAVVGEQFTLSCGPPWGHPEPTVSWKD 152
 Qy 175 GKPLAQFGRRHTVSGSLLMAREKXSD 202
 Db 153 GKPLAQFGRRHTVSGSLLMAREKXSD 180

RESULT 6

US-09-978-192A-211
 ; Sequence 211, Application US/09978192A
 ; Patent No. US2002017753A1
 ; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Deenoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630PIC9
 ; CURRENT APPLICATION NUMBER: US/09/978,192A
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 48.8%; Score 148; DB 9; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.1e-124;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 ASGQPPPTIRWLLNGQPLSNVPPDPHLLPDGTLTLLQPPARGHADGQALSTDLGVYTC 114
DQ 33 ASGQPPPTIRWLLNGQPLSNVPPDPHLLPDGTLTLLQPPARGHADGQALSTDLGVYTC 92
QY 115 EASNRLGTAVSRGARSVAVLREDFOIQPRDMVAVVGEQFTLECGPPWGHBPPTVSWNKD 174
DQ 93 EASNRLGTAVSRGARSVAVLREDFOIQPRDMVAVVGEQFTLECGPPWGHBPPTVSWNKD 152

QY 175 GKPLALQPGRHHTVSGGSLLMARAKSDE 202
DQ 153 GKPLALQPGRHHTVSGGSLLMARAKSDE 180

RESULT 7
US-09-999-832A-211
; Sequence 211, Application US/09999832A
; Publication No. US20020192706A1

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kllavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC63
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 48.8%; Score 148; DB 9; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.1e-124; Indels 0; Gaps 0;
Matches 148; Conservative 0; Mismatches 0

QY 55 ASGQPPPTIRLLNGPLSMVPPDPHLLPDGTLILLQPPARGHAHDGOALSTDIGVYTC 114
Db 33 ASGQPPPTIRLLNGPLSMVPPDPHLLPDGTLILLQPPARGHAHDGOALSTDIGVYTC 92
QY 115 EASNRLGTVASRGARLSAVLREDFOIQPRDMVAVVGEQFTLECGPPMGHPPTVSWWKD 174
Db 93 EASNRLGTVASRGARLSAVLREDFOIQPRDMVAVVGEQFTLECGPPMGHPPTVSWWKD 152
QY 175 GKPLALQPGRHVTSGGSLLMARAKSDE 202
Db 153 GKPLALQPGRHVTSGGSLLMARAKSDE 180

RESULT 8
US-09-978-189-211
; Sequence 211, Application US/09978189

Publication No. US20030004102A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
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PRIOR FILING DATE: 2001-07-30
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 / PRIOR APPLICATION NUMBER: 60/085573
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085704
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085697

Query Match 48.8%; Score 148; DB 10; Length 985;

Best Local Similarity 100.0%; Pred.No. 1.1e-124;

Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 ASGQPPPTIRLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAGHQAQALSTDLGYTC 114

Db 33 ASGQPPPTIRLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAGHQAQALSTDLGYTC 92

QY 115 EASNELGTAVSRGARGLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174

Db 93 EASNELGTAVSRGARGLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 152

QY 175 GKPLALQPGRTVSGGSLLMARAEKSD 202

Db 153 GKPLALQPGRTVSGGSLLMARAEKSD 180

RESULT 9

US-09-978-608A-211

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; Sequence 211, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978.608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 211
; LENGTH: 985
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-211

Query Match 48.8%; Score 148; DB 10; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.1e-124;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 ASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAHDGQALSTDLGVYTC 114
Db 33 ASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAHDGQALSTDLGVYTC 92

Qy 115 EASNRLGTAVSRGARLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174
Db 93 EASNRLGTAVSRGARLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 152

Qy 175 GKPLALQPGRHVTSGGSLLMARAEKSDE 202
Db 153 GKPLALQPGRHVTSGGSLLMARAEKSDE 180

RESULT 10
US-09-978-585A-211
; Sequence 211, Application US/09978585A
; Publication No. US20030049639A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978.585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 211
; LENGTH: 985
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-211

Query Match 48.8%; Score 148; DB 10; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.1e-124;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 ASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAHDGQALSTDLGVYTC 114
Db 33 ASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAHDGQALSTDLGVYTC 92

Qy 115 EASNRLGTAVSRGARLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174
Db 93 EASNRLGTAVSRGARLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 152

Qy 175 GKPLALQPGRHVTSGGSLLMARAEKSDE 202
Db 153 GKPLALQPGRHVTSGGSLLMARAEKSDE 180

RESULT 11
US-09-978-191A-211
; Sequence 211, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978.585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 211
; LENGTH: 985
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-211

Query Match 48.8%; Score 148; DB 10; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.1e-124;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 ASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAHDGQALSTDLGVYTC 114
Db 33 ASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAHDGQALSTDLGVYTC 92

Qy 115 EASNRLGTAVSRGARLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174
Db 93 EASNRLGTAVSRGARLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 152

Qy 175 GKPLALQPGRHVTSGGSLLMARAEKSDE 202
Db 153 GKPLALQPGRHVTSGGSLLMARAEKSDE 180

```

APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC4
CURRENT APPLICATION NUMBER: US/09/978,191A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
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PRIOR FILING DATE: 1998-03-12
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PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
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PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
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PRIOR APPLICATION NUMBER: 60/084639

; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 48.88; Score 148; DB 10; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.le-124; Indels 0; Gaps 0;
Matches 148; Conservative 0; Mismatches 0;

QY 55 ASGPPPTIRLWLNQPLSMVPPDPHLLPDGTLILLQPPARGHAGDQALSTDLGVYTC 114
Db 33 ASGPPPTIRLWLNQPLSMVPPDPHLLPDGTLILLQPPARGHAGDQALSTDLGVYTC 92
QY 115 EASNRLGTAVSRGARLSAVLRDEFQIQPRDMVAVVGEQTLTLCGPPWGHPEPTVSNWKD 174
Db 93 EASNRLGTAVSRGARLSAVLRDEFQIQPRDMVAVVGEQTLTLCGPPWGHPEPTVSNWKD 152
QY 175 GKPLALQPGHRTVSGGSLLMARAEKSD 202
Db 153 GKPLALQPGHRTVSGGSLLMARAEKSD 180

RESULT 12
US-09-978-403A-211
; Sequence 211, Application US/09978403A
; Publication No US20030050240A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC17
; CURRENT APPLICATION NUMBER: US/09/978,403A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085704
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085697

Query Match 48.8%; Score 148; DB 10; Length 985;

Best Local Similarity 100.0%; Pred. No. 1.le-124; Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	55	ASGQPPPTIRWLLNGOPLSMVPPDPHLLPDCGTLTLLQPPARGHADCQALSTDLGVYTC	114
Db	33	ASGQPPPTIRWLLNGOPLSMVPPDPHLLPDCGTLTLLQPPARGHADCQALSTDLGVYTC	92
QY	115	EASNLGTAVSRGARSVAVUREDFQIQPRDVAVVVGQFTLECGPPWGHPEPTVSWWKD	174
Db	93	EASNLGTAVSRGARSVAVUREDFQIQPRDVAVVVGQFTLECGPPWGHPEPTVSWWKD	152
QY	175	GKPLALQGRHTVSGSLLMARAEKSDE	202
Db	153	GKPLALQGRHTVSGSLLMARAEKSDE	180

RESULT 13

US-09-978-564A-211
 / Sequence 211, Application US/09978564A
 / Publication No. US20030050241A1
 / GENERAL INFORMATION:
 / APPLICANT: Ashkenazi, Avi
 / APPLICANT: Baker, Kevin P.
 / APPLICANT: Botstein, David
 / APPLICANT: Desnoyers, Luc
 / APPLICANT: Eaton, Dan
 / APPLICANT: Ferrara, Napoleon
 / APPLICANT: Filvaroff, Ellen
 / APPLICANT: Fong, Sherman
 / APPLICANT: Gao, Wei-Qiang
 / APPLICANT: Gerber, Hanspeter
 / APPLICANT: Gerritsen, Mary E.
 / APPLICANT: Goddard, Audrey
 / APPLICANT: Godowski, Paul J.
 / APPLICANT: Grimaldi, J. Christopher
 / APPLICANT: Gurney, Austin L.
 / APPLICANT: Hillan, Kenneth J.
 / APPLICANT: Kljavin, Ivar J.

; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084639
 ; PRIOR FILING DATE: 1998-05-07
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 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 48.8%; Score 148; DB 10; Length 985;
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Qy	115	EASNLGTVASRGARLSAVLRDFOQPRDMVAVVGEOFTLECGPPWGHPEPTVSNWKD	174
Db	93	EASNLGTVASRGARLSAVLRDFOQPRDMVAVVGEOFTLECGPPWGHPEPTVSNWKD	152
Qy	175	GKPLALQPGRHTVSGGSLLMARAEKSDE	202
Db	153	GKPLALQPGRHTVSGGSLLMARAEKSDE	180

RESULT 14
 US-09-999-833A-211
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 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrata, Napoleon
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 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630PIC65
 ; CURRENT APPLICATION NUMBER: US/09/999,833A
 ; CURRENT FILING DATE: 2001-10-24
 ; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 48.8%; Score 148; DB 10; Length 985;

Best Local Similarity 100.0%; Pred. No. 1.e-124; Indels 0; Gaps 0;
Matches 148; Conservative 0; Mismatches 0;

QY 55 ASGQPPPTIRLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHARDGOALSTDIGVYTC 114
DB 33 ASGQPPPTIRLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHARDGOALSTDIGVYTC 92
QY 115 EASNELGTAVSGCARLSVAVLRDFOIQPRDMVAVVVGQFTLECGPPHGHPEPTVSWWKD 174
DB 93 EASNELGTAVSGCARLSVAVLRDFOIQPRDMVAVVVGQFTLECGPPHGHPEPTVSWWKD 152
QY 175 GKPLALQPGHRTVSGSLIMAPAEKSDE 202
DB 153 GKPLALQPGHRTVSGSLIMAPAEKSDE 180

RESULT 15

US-09-981-915A-211
; Sequence 211, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC12
CURRENT APPLICATION NUMBER: US/09/981,915A
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 1997-10-17
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Query Match      48.8%; Score 148; DB 10; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.le-124;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 ASGQPPPTIRLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAHDGQALSTDLGVYTC 114
Db 33 ASGQPPPTIRLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAHDGQALSTDLGVYTC 92

Qy 115 EASNRLGTAVSGRGARLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174
Db 93 EASNRLGTAVSGRGARLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 152

Qy 175 GKPLALQGRHTVSGSLLIMARAEKSDR 202
Db 153 GKPLALQGRHTVSGSLLIMARAEKSDR 180

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Search completed: February 29, 2004, 08:23:55
Job time : 56 secs

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204	4	US-09-252-991A-30186

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Sequence 2, Appli
Sequence 2, Appli

Sequence 10, Appl

Sequence 10, Appl

Sequence 2, Appli

References

Applying and Using Sar

Curriculum

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; TYPE: PRT
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; NAME/KEY: UNSURE
; LOCATION: -16
; OTHER INFORMATION: Xaa = Ala,Gly
US-09-621-976-4124

Query Match 2.6%; Score 8; DB 4; Length 118;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 98 SLPLLLLL 105

RESULT 3
US-09-673-395A-577
; Sequence 577, Application US/09673395A
; Patent No. 6620923
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
; FILE REFERENCE: ALBRE-12
; CURRENT APPLICATION NUMBER: US/09/673.395A
; CURRENT FILING DATE: 2000-10-17
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US-09-673-395A-577

Query Match 2.6%; Score 8; DB 4; Length 161;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 2 LPLLLLLL 9

RESULT 4
US-08-837-029-2
; Sequence 2, Application US/08837029
; Patent No. 5945303
; GENERAL INFORMATION:
; APPLICANT: Wei et al.
; TITLE OF INVENTION: Human Hematopoietic - Specific Protein
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,029
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US96/04930
; FILING DATE: 11-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 189 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-837-029-2

Query Match 2.6%; Score 8; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 SLPLLLLL 21
DB 4 SLPLLLLL 11

RESULT 5
US-09-800-729-114
; Sequence 114, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P204P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 114
; LENGTH: 287
; TYPE: PRT

```

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; ORGANISM: Homo sapiens
US-09-800-729-114

Query Match      2.6%; Score 8; DB 4; Length 287;
Best Local Similarity 100.0%; Pred. No. 16;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 SLPLLLLL 21
DB      12 SLPLLLLL 19

RESULT 6
US-09-800-729-153
; Sequence 153, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 153
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-153

Query Match      2.6%; Score 8; DB 4; Length 287;
Best Local Similarity 100.0%; Pred. No. 16;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 SLPLLLLL 21
DB      12 SLPLLLLL 19

RESULT 7
US-09-615-192A-284
; Sequence 284, Application US/09615192A
; Patent No. 6410718
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; TITLE OF INVENTION: Modification of Plant Lignin Content
; FILE REFERENCE: 11000.100304U
; CURRENT APPLICATION NUMBER: US/09/615,192A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/713,000
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 284
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-615-192A-284

Query Match      2.6%; Score 8; DB 4; Length 330;
Best Local Similarity 100.0%; Pred. No. 18;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 SLPLLLLL 21
DB      12 SLPLLLLL 19

RESULT 8
US-09-800-729-82
; Sequence 82, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 82
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-82

Query Match      2.6%; Score 8; DB 4; Length 613;
Best Local Similarity 100.0%; Pred. No. 32;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 SLPLLLLL 21
DB      12 SLPLLLLL 19

RESULT 9
US-09-800-729-98
; Sequence 98, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 98
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (507)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-800-729-98

Query Match      2.6%; Score 8; DB 4; Length 613;
Best Local Similarity 100.0%; Pred. No. 32;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 SLPLLLLL 21
DB      12 SLPLLLLL 19

RESULT 10
US-08-447-464-3
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Sequence 3, Application US/08447464
Patent No. 5840842
GENERAL INFORMATION:
APPLICANT: Schllessinger, Joseph
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN
TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGMA
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,464
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/130,570
FILING DATE: 01-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-043
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1501 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-447-464-3

Query Match 2.6%; Score 8; DB 2; Length 1501;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 207 CVATNSAG 214
Db 207 CVATNSAG 214

RESULT 11
US-08-716-679-3
Sequence 3, Application US/08716679
Patent No. 5846800
GENERAL INFORMATION:
APPLICANT: Schllessinger, Joseph
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN
TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGMA
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,679
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/130,570
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-043
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1501 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-716-679-3

Query Match 2.6%; Score 8; DB 2; Length 1501;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 207 CVATNSAG 214
Db 207 CVATNSAG 214

RESULT 12
US-08-348-006B-5
Sequence 5, Application US/08348006B
Patent No. 5658756
GENERAL INFORMATION:
APPLICANT: RODAN, GIDEON A.
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: J. MARK HAND
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
CITY: RAYWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,006B
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,032
FILING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: HAND, J., MARK
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 189921A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3905
TELEFAX: 908-594-4720
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1911 amino acids

```
/
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-348-006B-5

Query Match      2.6%; Score 8; DB 1; Length 1911;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      207 CVATNSAG 214
Db      207 CVATNSAG 214

RESULT 13
US-08-800-825A-5
; Sequence 5, Application US/08800825A
; Patent No. 5866397
; GENERAL INFORMATION:
; APPLICANT: RODAN, GIDEON A.
; APPLICANT: SCHMIDT, AZRIEL
; TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/158.657
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/800,825
; FILING DATE: 14-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: HAND, J. MARK
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18992DA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-4720
; TELEFAX: 732-594-3905
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1911 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-158-657-5

Query Match      2.6%; Score 8; DB 3; Length 1911;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      207 CVATNSAG 214
Db      207 CVATNSAG 214

RESULT 15
PCT-US94-10166-5
; Sequence 5, Application PC/TUS9410166
; GENERAL INFORMATION:
; APPLICANT: RODAN, GIDEON A
; APPLICANT: SCHMIDT, AZRIEL
; APPLICANT: RUTLEDGE, SU JANE
; TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JOHN W. WALLEN III
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVE.
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10166
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/ FILING DATE: 09-SEPT-1994
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/122,032
/ FILING DATE: 14-SEP-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: WALLEN, JOHN W III
/ REGISTRATION NUMBER: 35403
/ REFERENCE/DOCKET NUMBER: 18992
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 908-594-3905
/ TELEFAX: 908-594-4720
/ TELEX: 138825
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1911 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
PCT-US94-10166-5

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Query Match      2.6%; Score 8; DB 5; Length 1911;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      207 CVATNSAG 214
      |||||
DB      207 CVATNSAG 214

```

Search completed: February 29, 2004, 08:19:35
Job time : 25 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 27, 2004, 15:39:59 ; Search time 76 Seconds
(without alignments)
1126.472 Million cell updates/sec

Title: US-10-047-021-86

Perfect score: 303

Sequence: 1 MGSGDLSLGGRLPLLL.....SGPRLPREARELRGQRNTG 303

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	300	99.0	303	5	ABP62033 Human sec
2	300	99.0	304	2	RAY12934 Amino aci
3	148	48.8	480	4	AAU00501 Human TAN
4	148	48.8	985	2	RAY41716 Human PRO
5	148	48.8	985	3	ABAB4272 Human PRO
6	148	48.8	985	6	ABO25218 Novel hum
7	148	48.8	985	6	ABU72224 Novel hum
8	148	48.8	985	6	ABU84904 Human sec
9	148	48.8	985	6	ABU61102 Human PRO
10	148	48.8	985	6	ABU80371 Human sec
11	148	48.8	985	6	ADA24750 Novel hum
12	148	48.8	985	6	ABO19673 Human sec
13	148	48.8	985	6	ADA12411 Human sec
14	148	48.8	985	6	ABO19564 Novel hum
15	148	48.8	985	7	ADB73717 Human PRO
16	148	48.8	985	7	ADB76433 Human PRO
17	148	48.8	985	7	ADC43859 Human sec
18	148	48.8	985	7	ADC61619 Human sec
19	148	48.8	985	7	ADC63583 Human sec
20	148	48.8	985	7	ADC65683 Human sec
21	148	48.8	985	7	ADC68807 Human sec
22	148	48.8	985	7	ADC62867 Human sec
23	148	48.8	985	7	ADC67932 Human sec
24	148	48.8	985	7	ADC41252 Human sec
25	148	48.8	985	7	ADC67307 Human sec

ALIGNMENTS

RESULT 1

ABP62033

ID ABP62033 standard; protein; 303 AA.

XX AC ABP62033;

DT 12-NOV-2002 (first entry)

DE Human secreted protein SEQ ID NO 86.

XX KW Human; nontropic; neuroprotective; cytostatic; dermatological; virucide;
 KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
 KW antiparkinsonian; antistickling; antianaemic; antiarthritic; cancer;
 KW antirheumatic; hepatotropic; cerebrotective; antiinflammatory;
 KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
 KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine.

XX OS Homo sapiens.

XX XX WO200257420-A2.

XX PD 25-JUL-2002.

XX PF 17-JAN-2002; 2002WO-US001109.

XX PR 18-JAN-2001; 2001US-0262066P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Moore PA, Ruben SM, Lafleur DW, Shi Y, Rosen CA, Olsen H;

XX PI Ebner R, Brewer LA;

XX DR WPI: 2002-599716/54.

XX DR N-PSDB; ABQ92573.

XX PT New polynucleotides and polypeptides useful for diagnosing, prognosing,
 PT treating or preventing e.g. neurodegenerative, central nervous system,
 PT autoimmune, respiratory, reproductive, or inflammatory diseases or
 PT disorders.

XX PS Claim 11; Fig 1; 785pp; English.

XX CC The invention relates to novel genes (ABQ92553-ABQ92607) and proteins
 CC (ABP62013-ABP62153) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in

26	148	48.8	985	7	ADC62243	Human sec
27	148	48.8	985	7	ADC41876	Human sec
28	148	48.8	985	7	ADE49245	Human sec
29	148	48.8	985	7	ADE35299	Human sec
30	148	48.8	985	7	ADE16413	Human sec
31	148	48.8	985	7	ADD73028	Human sec
32	148	48.8	985	7	ADD72386	Human sec
33	148	48.8	985	7	ADE17037	Human sec
34	148	48.8	985	7	ADE48545	Human sec
35	148	48.8	985	7	ADE89646	Human sec
36	148	48.8	1007	5	ABB97310	Novel hum
37	148	48.8	1104	5	AAU99419	Human ECS
38	120	39.6	792	4	AAU99515	Human pro
39	120	39.6	792	4	AAU99515	Amino aci
40	110	36.3	934	4	AAU00500	Human TAN
41	27	8.9	1015	5	AAU99420	Mouse ECS
42	20	6.6	20	5	AAU99411	Human ECS
43	19	6.3	64	3	AAU99411	Human S,
44	12	4.0	12	5	AAU99410	Human ECS
45	10	3.3	10	5	AAU99412	Human ECS

CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemia; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections

XX
 SQ Sequence 303 AA;
 Query Match 99.0%; Score 300; DB 5; Length 303;
 Best Local Similarity 100.0%; Pred. No. 1e-273;
 Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSGGDSLLGGRGSLPLLLLLIMGMAQDSPQILVHPQDLFGPGPARMSCRASGQPP 60
 DB 1 MSGGDSLLGGRGSLPLLLLLIMGMAQDSPQILVHPQDLFGPGPARMSCRASGQPP 60
 QY 61 PTIRWLLNGQPLSMVPPDPHLLPDGTLTLLQPPARGHAGDQALSTDLGVYTCESNRL 120
 DB 61 PTIRWLLNGQPLSMVPPDPHLLPDGTLTLLQPPARGHAGDQALSTDLGVYTCESNRL 120
 QY 121 GTAVSRGARLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKGKPLAL 180
 DB 121 GTAVSRGARLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKGKPLAL 180
 QY 181 QPGRHTVSGGSLLMARAEKSDXTYMCVATNSAGHRSRAARVSIQPDYTEPVELLAV 240
 DB 181 QPGRHTVSGGSLLMARAEKSDXTYMCVATNSAGHRSRAARVSIQPDYTEPVELLAV 240
 QY 241 RIQLENTVLLNPDPAEGPKPRPAVLWKVSGPXRLPNLTPCSPGPRLPREARELRGQR 300
 DB 241 RIQLENTVLLNPDPAEGPKPRPAVLWKVSGPXRLPNLTPCSPGPRLPREARELRGQR 300
 QY 301 NTG 303
 DB 301 NTG 303

RESULT 2

AA12934

ID AA12934 standard; protein; 304 AA.

AC AA12934;

XX 17-JUN-1999 (first entry)

XX Amino acid sequence of a human secreted peptide.

DE Human secreted protein; cancer; immune disorder; infection;
 XX inflammatory disorder; skin disorder; tumour; atherosclerosis;
 KW restenosis; autoimmune disorder; Alzheimer's disease;
 KW peripheral neuropathy; trauma; spinal cord injury; allergy;
 KW hematopoietic disorder; skeletal disorder; neurological disorder;
 KW arthritic disorder; asthma; immunodeficiency disease; AIDS;
 KW transplant rejection; ss.

XX Homo sapiens.

OS Key

FH Location/Qualifiers

FT Peptide

FT 1..27

FT /note= "signal peptide"

FT Protein

FT 28..303

FT /note= "secreted protein"

XX WO9911293-A1.

XX 11-MAR-1999.

XX 03-SEP-1998; 98WO-US018360.

XX

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XX

XX

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XX

XX

XX

XX

XX 05-SEP-1997; 97US-0057626P.
 PR 05-SEP-1997; 97US-0057663P.
 PR 05-SEP-1997; 97US-0057669P.
 PR 12-SEP-1997; 97US-0058666P.
 PR 12-SEP-1997; 97US-0058667P.
 PR 12-SEP-1997; 97US-0058973P.
 PR 12-SEP-1997; 97US-0058974P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Moore PA, Ruben SM, Lafleur DW, Shi Y, Rosen GA, Olsen HS;
 PI Ebner R, Brewer LA;
 XX
 DR WPI: 1999-204988/17.
 DR N-PSDB; AAX51721.
 XX
 PT New isolated human genes and the secreted polypeptides they encode -
 PT useful for diagnosis and treatment of e.g. neurological disorders,
 PT tumors, immune disorders, inflammation or hematological disorders.
 XX
 PS Claim 11; Page 190-191; 215pp; English.
 XX
 CC AAY12914-68 represent human secreted proteins. The polypeptides and their
 CC corresponding polynucleotides are useful for preventing, treating or
 CC ameliorating medical conditions, e.g. by protein or gene therapy.
 CC Pathological conditions can also be diagnosed by determining the amount
 CC of the new polypeptides in a sample or by determining the presence of
 CC mutations in the new polynucleotides. Specific uses are described for
 CC each polynucleotide, based on which tissues they are most highly
 CC expressed in, and include developing products for the diagnosis or
 CC treatment of cancer, immune disorders, infection, inflammatory disorders,
 CC skin disorders, tumours, atherosclerosis, restenosis, trauma, spinal
 CC cord injuries, Alzheimer's disease, peripheral neuropathies, skeletal disorders,
 CC neurological disorders, allergic, hematopoietic disorders, arthritic disorders,
 CC diseases, AIDS and transplant rejection. The polypeptides are also useful
 CC for identifying their binding partners
 XX
 SQ Sequence 304 AA;
 Query Match 99.0%; Score 300; DB 2; Length 304;
 Best Local Similarity 100.0%; Pred. No. 1e-273;
 Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSGGDSLLGGRGSLPLLLLLIMGMAQDSPQILVHPQDLFGPGPARMSCRASGQPP 60
 DB 1 MSGGDSLLGGRGSLPLLLLLIMGMAQDSPQILVHPQDLFGPGPARMSCRASGQPP 60
 QY 61 PTIRWLLNGQPLSMVPPDPHLLPDGTLTLLQPPARGHAGDQALSTDLGVYTCESNRL 120
 DB 61 PTIRWLLNGQPLSMVPPDPHLLPDGTLTLLQPPARGHAGDQALSTDLGVYTCESNRL 120
 QY 121 GTAVSRGARLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKGKPLAL 180
 DB 121 GTAVSRGARLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKGKPLAL 180
 QY 181 QPGRHTVSGGSLLMARAEKSDXTYMCVATNSAGHRSRAARVSIQPDYTEPVELLAV 240
 DB 181 QPGRHTVSGGSLLMARAEKSDXTYMCVATNSAGHRSRAARVSIQPDYTEPVELLAV 240
 QY 241 RIQLENTVLLNPDPAEGPKPRPAVLWKVSGPXRLPNLTPCSPGPRLPREARELRGQR 300
 DB 241 RIQLENTVLLNPDPAEGPKPRPAVLWKVSGPXRLPNLTPCSPGPRLPREARELRGQR 300
 QY 301 NTG 303
 DB 301 NTG 303

RESULT 3

AAU0501

ID AAU0501 standard; protein; 480 AA.

XX AAU00501;
 XX 18-JUL-2001 (first entry)
 XX Human TANGO 330 form 2 protein.
 XX
 XX Human; TANGO 315; clone Jthx181e12; TANGO 330; TANGO 437; TANGO 480;
 XX cellular process regulator; gene therapy; astrocyte; cancer; Roundabout;
 XX adrenal cortex; hypoadrenalism; hyperadrenalism; neoplasia;
 XX cell proliferative disorder; neurological disorder; Alzheimer's disease.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX Peptide 1..20
 XX /label= signal_peptide
 XX Modified-site 15..17
 XX /note= "Protein kinase C phosphorylation site"
 XX Domain 21..480
 XX /label= Extracellular_domain
 XX Protein 21..480
 XX /label= Mature_TANGO_330_form_2_protein
 XX Modified-site 30..33
 XX /note= "cAMP and cGMP dependent protein kinase
 XX phosphorylation site"
 XX Modified-site 44..47
 XX Domain 77..147
 XX /label= Ig-like_domain
 XX Modified-site 93..95
 XX /note= "Protein kinase C phosphorylation site"
 XX Modified-site 100..105
 XX /note= "N-myristylation site"
 XX Modified-site 133..138
 XX /note= "N-myristylation site"
 XX Modified-site 141..146
 XX /note= "N-myristylation site"
 XX Modified-site 148..150
 XX /note= "Protein kinase C phosphorylation site"
 XX Modified-site 152..157
 XX /note= "N-myristylation site"
 XX Modified-site 158..163
 XX /note= "N-myristylation site"
 XX Domain 182..240
 XX /label= Ig-like_domain
 XX Modified-site 230..236
 XX /note= "Tyrosine kinase phosphorylation site"
 XX Modified-site 234..239
 XX /note= "N-myristylation site"
 XX Modified-site 255..258
 XX /note= "Casein kinase II phosphorylation site"
 XX Modified-site 277..280
 XX /note= "Asn is N-glycosylated"
 XX Modified-site 298..300
 XX /note= "Protein kinase C phosphorylation site"
 XX Modified-site 325..330
 XX /note= "N-myristylation site"
 XX Modified-site 343..348
 XX /note= "N-myristylation site"
 XX Modified-site 358..360
 XX /note= "Protein kinase C phosphorylation site"
 XX Modified-site 386..388
 XX /note= "Protein kinase C phosphorylation site"
 XX Modified-site 391..394
 XX /note= "Asn is N-glycosylated"
 XX Modified-site 408..413
 XX /note= "N-myristylation site"
 XX Modified-site 420..423
 XX /note= "Asn is N-glycosylated"
 XX Modified-site 427..430
 XX /note= "Asn is N-glycosylated"
 XX Modified-site 435..438

FT /note= "Casein kinase II phosphorylation site"
 FT 456..461
 FT /note= "N-myristylation site"
 XX
 XX WO200123523-A2.
 XX
 XX 05-APR-2001.
 XX
 XX 02-OCT-2000; 2000WO-US027202.
 XX
 XX 30-SEP-1999; 99US-00409634.
 XX
 XX (MILL-) MILLENNIUM PHARM INC.
 XX
 XX Kirst S, Wrighton N, Fraser CC;
 XX WPI; 2001-235372/24.
 XX N-PSDB; AAS01695.
 XX
 XX Isolated secreted proteins and their encoding nucleic acids are used for
 XX diagnosis and treatment of e.g. bacterial and viral infections,
 XX autoimmune diseases and inflammatory disorders.
 XX
 XX Claim 9; Fig 14; 261pp; English.
 XX
 XX The present sequence representing human TANGO 330 form 2 is isolated from
 XX cDNA clone Jthx181e12 from a human astrocyte cDNA library. TANGO 330 is
 XX 1 of 4 novel human transmembrane proteins which also includes TANGO 315
 XX (AAU00498-AAU00499), TANGO 437 (AAU00502) and TANGO 480 (AAU00503). The
 XX nucleic acids encoding these proteins are useful as modulating agents in
 XX regulating a variety of cellular processes and can be used to express the
 XX proteins in a host cell in gene therapy applications. Antisense nucleic
 XX acid molecules and expression vectors containing the TANGO nucleic acids
 XX are also described. Diagnostic assays can be used to detect genetic
 XX alterations in the TANGO nucleic acids and to identify compounds that
 XX bind to or modulate activity of the TANGO proteins. Anti-TANGO antibodies
 XX are used diagnostically to monitor protein levels in tissue as a clinical
 XX testing procedure. TANGO 330 shows homology to human Roundabout. TANGO
 XX 330 nucleic acids and proteins may be used to diagnose, treat and monitor
 XX disorders of the adrenal cortex e.g. hypoadrenalism, hyperadrenalism, and
 XX neoplasia. They can also be used to treat cell proliferative disorders
 XX (e.g. cancer), and neurological disorders e.g. Alzheimer's disease
 XX
 XX Sequence 480 AA;
 XX
 XX Query Match 48.8%; Score 148; DB 4; Length 480;
 XX Best Local Similarity 100.0%; Pred. No. 1.9e-130;
 XX Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 55 ASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGTLILQPPARGHAHDGQALSTDLGVYTC 114
 Db 86 ASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGTLILQPPARGHAHDGQALSTDLGVYTC 145
 Qy 115 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVVGEOFTLECGPPWGHGPEPTVSWWKD 174
 Db 146 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVVGEOFTLECGPPWGHGPEPTVSWWKD 205
 Qy 175 GKPLALQPGRHVTGSGSLLMARAESKDE 202
 Db 206 GKPLALQPGRHVTGSGSLLMARAESKDE 233
 RESULT 4
 ID AAY41716
 XX AAY41716 standard; protein; 985 AA.
 XX AC AAY41716;
 XX
 XX 07-DEC-1999 (first entry)
 XX Human PRO860 protein sequence.
 DE Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
 KW

KW probe: blood coagulation disorder; cancer; cellular adhesion disorder;
 KW secreted protein; transmembrane protein.

XX Homo sapiens.
 OS WO9946281-A2.
 PN
 PD 16-SEP-1999.
 XX
 XX
 XX 08-MAR-1999; 99WO-US0505028.
 XX
 XX 10-MAR-1998; 98US-00774502P.
 PR 11-MAR-1998; 98US-0077632P.
 PR 11-MAR-1998; 98US-0077641P.
 PR 11-MAR-1998; 98US-0077649P.
 PR 12-MAR-1998; 98US-0077791P.
 PR 13-MAR-1998; 98US-0078004P.
 PR 17-MAR-1998; 98US-00040220.
 PR 20-MAR-1998; 98US-0078886P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 20-MAR-1998; 98US-0078936P.
 PR 20-MAR-1998; 98US-0078939P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 26-MAR-1998; 98US-0079565P.
 PR 27-MAR-1998; 98US-0079663P.
 PR 27-MAR-1998; 98US-0079664P.
 PR 27-MAR-1998; 98US-0079689P.
 PR 27-MAR-1998; 98US-0079728P.
 PR 30-MAR-1998; 98US-0079786P.
 PR 30-MAR-1998; 98US-0079920P.
 PR 31-MAR-1998; 98US-0079923P.
 PR 31-MAR-1998; 98US-0080105P.
 PR 31-MAR-1998; 98US-0080107P.
 PR 31-MAR-1998; 98US-0080165P.
 PR 31-MAR-1998; 98US-0080194P.
 PR 01-APR-1998; 98US-0080327P.
 PR 01-APR-1998; 98US-0080328P.
 PR 01-APR-1998; 98US-0080333P.
 PR 01-APR-1998; 98US-0080334P.
 PR 08-APR-1998; 98US-0081049P.
 PR 08-APR-1998; 98US-0081070P.
 PR 08-APR-1998; 98US-0081071P.
 PR 09-APR-1998; 98US-0081195P.
 PR 09-APR-1998; 98US-0081203P.
 PR 09-APR-1998; 98US-0081229P.
 PR 15-APR-1998; 98US-0081817P.
 PR 15-APR-1998; 98US-0081838P.
 PR 15-APR-1998; 98US-0081952P.
 PR 15-APR-1998; 98US-0081955P.
 PR 21-APR-1998; 98US-0082568P.
 PR 21-APR-1998; 98US-0082569P.
 PR 22-APR-1998; 98US-0082700P.
 PR 22-APR-1998; 98US-0082704P.
 PR 22-APR-1998; 98US-0082804P.
 PR 23-APR-1998; 98US-0082767P.
 PR 23-APR-1998; 98US-0082796P.
 PR 27-APR-1998; 98US-0083336P.
 PR 28-APR-1998; 98US-0083342P.
 PR 29-APR-1998; 98US-0083392P.
 PR 29-APR-1998; 98US-0083495P.
 PR 29-APR-1998; 98US-0083496P.
 PR 29-APR-1998; 98US-0083499P.
 PR 29-APR-1998; 98US-0083500P.
 PR 29-APR-1998; 98US-0083545P.
 PR 29-APR-1998; 98US-0083546P.
 PR 29-APR-1998; 98US-0083558P.
 PR 29-APR-1998; 98US-0083559P.
 PR 30-APR-1998; 98US-0083742P.
 PR 06-MAY-1998; 98US-0084366P.
 PR 06-MAY-1998; 98US-0084414P.
 PR 07-MAY-1998; 98US-0084411P.
 PR 07-MAY-1998; 98US-0084598P.
 PR 07-MAY-1998; 98US-0084600P.
 PR
 PR 07-MAY-1998; 98US-0084627P.
 PR 07-MAY-1998; 98US-0084637P.
 PR 07-MAY-1998; 98US-0084639P.
 PR 07-MAY-1998; 98US-0084640P.
 PR 07-MAY-1998; 98US-0084643P.
 PR 13-MAY-1998; 98US-0085323P.
 PR 13-MAY-1998; 98US-0085338P.
 PR 13-MAY-1998; 98US-0085339P.
 PR 15-MAY-1998; 98US-0085573P.
 PR 15-MAY-1998; 98US-0085579P.
 PR 15-MAY-1998; 98US-0085580P.
 PR 15-MAY-1998; 98US-0085582P.
 PR 15-MAY-1998; 98US-0085689P.
 PR 15-MAY-1998; 98US-0085697P.
 PR 15-MAY-1998; 98US-0085700P.
 PR 18-MAY-1998; 98US-0085704P.
 PR 22-MAY-1998; 98US-0086023P.
 PR 22-MAY-1998; 98US-0086392P.
 PR 22-MAY-1998; 98US-0086414P.
 PR 22-MAY-1998; 98US-0086430P.
 PR 28-MAY-1998; 98US-0086486P.
 PR 28-MAY-1998; 98US-0087098P.
 PR 28-MAY-1998; 98US-0087106P.
 PR 30-JUL-1998; 98US-0087208P.
 PR 11-SEP-1998; 98US-0094651P.
 PR 11-SEP-1998; 98US-0100038P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
 PI WPI; 1999-551358/46.
 XX N-PSDB; AA234069.
 DR
 DR
 XX
 PT New secreted and transmembrane polypeptides and their polynucleotides,
 PT useful for treating blood coagulation disorders, cancers and cellular
 PT adhesion disorders.
 PT
 XX
 PS Claim 12; Fig 77; 530pp; English.
 XX
 XX The present invention describes secreted and transmembrane polypeptides
 CC and their polynucleotides. The nucleotide sequences are useful as sources
 CC of probes, primers, for chromosome mapping, and for generation of
 CC antisense sequences. They can also be used to create transgenic animals.
 CC The proteins can be used to treat a variety of diseases and disorders,
 CC depending on their function. Diseases that may be treated include blood
 CC coagulation disorders, cancers and cellular adhesion disorders. They may
 CC also be used to raise antibodies. AA233891 to AA234338, and AA41685 to
 CC AA41774 represent polynucleotide and polypeptide sequence given in the
 CC exemplification of the present invention
 XX
 XX Sequence 985 AA;
 SQ
 Query Match 48.8%; Score 148; DB 2; Length 985;
 Best Local Similarity 100.0%; Pred. No. 3.5e-130; Indels 0; Gaps 0;
 Matches 148; Conservative 0; Mismatches 0;
 QY 55 ASGQPPPTIRLLNGQPLSMVPPDPHLLPDGTLTLLQPPARGHAHQALSTDLGVYTC 114
 DB 33 ASGQPPPTIRLLNGQPLSMVPPDPHLLPDGTLTLLQPPARGHAHQALSTDLGVYTC 92
 QY 115 EASNLGTAVSGRGARLSVAVLRDFQIPQPRDMVAVGEOPTLECPGPGHPEPTVSNWKD 174
 DB 93 EASNLGTAVSGRGARLSVAVLRDFQIPQPRDMVAVGEOPTLECPGPGHPEPTVSNWKD 152
 QY 175 GKPLALQFGRHTVSGGSLLMARAEKSDE 202
 DB 153 GKPLALQFGRHTVSGGSLLMARAEKSDE 180
 RESULT 5
 AAB44272
 ID AAB44272 standard; protein; 985 AA.

XX	AA44272;	Db	33	ASGQPPPTIRWLNGQPLSMVPPDPHLLPDGTLTLLQPPARGHAHQALSTDLGVYTC	92
AC					
XX	08-FEB-2001 (first entry)	QY	115	EASNRLGTAARGARLSVAVLRDFQIQPRDMVAVGEGQFTLECGPPMGHPEPTVSWWKD	174
DT					
XX	Human PR0860 (UNQ421) protein sequence SEQ ID NO:211.	Db	93	EASNRLGTAARGARLSVAVLRDFQIQPRDMVAVGEGQFTLECGPPMGHPEPTVSWWKD	152
DE					
XX	Human; secreted protein; transmembrane protein; PRO; EST; cytosstatic;	QY	175	GKPLALQPRHTVSGSLLMARAESKDE	202
KW	expressed sequence tag; detection; cancer.				
KW		Db	153	GKPLALQPRHTVSGSLLMARAESKDE	180
XX	Homo sapiens.				
OS					
XX	WO200053756-A2.				
PN					
XX	14-SEP-2000.				
XX					
XX	18-FEB-2000; 2000WO-US004341.				
XX					
PR	08-MAR-1999; 99WO-US005028.				
PR	12-MAR-1999; 99US-0123957P.				
PR	29-MAR-1999; 99US-0126773P.				
PR	21-APR-1999; 99US-0130232P.				
PR	28-APR-1999; 99US-0131445P.				
PR	14-MAY-1999; 99US-0134287P.				
PR	23-JUN-1999; 99US-0141037P.				
PR	26-JUL-1999; 99US-0145698P.				
PR	29-OCT-1999; 99US-0162506P.				
PR	30-NOV-1999; 99WO-US028213.				
PR	02-DEC-1999; 99WO-US028551.				
PR	16-DEC-1999; 99WO-US030095.				
PR	30-DEC-1999; 99WO-US031243.				
PR	30-DEC-1999; 99WO-US031274.				
PR	05-JAN-2000; 2000WO-US000219.				
PR	06-JAN-2000; 2000WO-US000377.				
PR	06-JAN-2000; 2000WO-US000376.				
XX	(GETH) GENENTECH INC.				
XX					
PI	Askenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;				
PI	Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;				
PI	Goddard A, Godowski P, Grimaldi CT, Gurney AL, Hillan KJ;				
PI	Klijavin IU, Kuo SS, Napier MA, Pan J, Faoni NF, Roy MA, Shelton DL;				
PI	Stewart TA, Tumas D, Williams PM, Wood WI;				
XX	WPI; 2000-611443/58.				
DR	N-PSDB; AAC78502.				
XX					
PT	Novel PRO polypeptides and polynucleotides used in detection methods, to				
PT	target bioactive molecules to specific cells, and to modulate cellular				
PT	activities.				
XX					
PS	Claim 12; Fig 77; 636pp; English.				
XX					
CC	AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence				
CC	tag) sequences which encode secreted or transmembrane PRO polypeptides.				
CC	The PRO polynucleotides and polypeptides have cytosstatic activity. The				
CC	polynucleotides and polypeptides can be used for detecting the presence				
CC	of PRO polypeptides in samples, for linking bioactive molecules to cells				
CC	and for modulating biological activities of cells, using the polypeptides				
CC	for specific targeting. The polypeptide targeting can be used to kill the				
CC	target cells, e.g. for the treatment of cancers. The polypeptide pairs				
CC	provide specific targeting of bioactive molecules to cells. AAC78600 to				
CC	AAC78987 represent PCR primers and probes used in the isolation of the				
CC	PRO polynucleotide sequences				
XX					
SQ	Sequence' 985 AA;				
	Query Match 48.8%; Score 148; DB 3; Length 985;				
	Best Local Similarity 100.0%; Pred. No. 3.5e-130; Indels 0; Gaps 0;				
	Matches 148; Conservative 0; Mismatches 0;				
QY	55 ASGQPPPTIRWLNGQPLSMVPPDPHLLPDGTLTLLQPPARGHAHQALSTDLGVYTC				114

PR	15-APR-1998;	98US-0081819P.	PR	12-MAR-1999;	99US-00267213.
PR	15-APR-1998;	98US-0081838P.	PR	12-MAR-1999;	99US-0123857P.
PR	15-APR-1998;	98US-0081952P.	PR	29-MAR-1999;	99US-0126773P.
PR	15-APR-1998;	98US-0081955P.	PR	12-APR-1999;	99US-00284291.
PR	21-APR-1998;	98US-0082568P.	PR	21-APR-1999;	99US-0130232P.
PR	21-APR-1998;	98US-0082569P.	PR	26-APR-1999;	99US-0131022P.
PR	22-APR-1998;	98US-0082700P.	PR	28-APR-1999;	99US-0131445P.
PR	22-APR-1998;	98US-0082707P.	PR	14-MAY-1999;	99US-00311832.
PR	22-APR-1998;	98US-0082797P.	PR	14-MAY-1999;	99US-0134287P.
PR	23-APR-1998;	98US-0082804P.	PR	14-MAY-1999;	99WO-US010733.
PR	23-APR-1998;	98US-0082796P.	PR	02-JUN-1999;	99WO-US012252.
PR	26-APR-1998;	98US-0083336P.	PR	16-JUN-1999;	99US-0139557P.
PR	29-APR-1998;	98US-0083322P.	PR	23-JUN-1999;	99US-0141037P.
PR	29-APR-1998;	98US-0083392P.	PR	07-JUL-1999;	99US-0142680P.
PR	29-APR-1998;	98US-0083495P.	PR	26-JUL-1999;	99US-0145698P.
PR	29-APR-1998;	98US-0083499P.	PR	28-JUL-1999;	99US-0146222P.
PR	29-APR-1998;	98US-0083500P.	PR	25-AUG-1999;	99US-00380137.
PR	29-APR-1998;	98US-0083545P.	PR	25-AUG-1999;	99US-00380138.
PR	29-APR-1998;	98US-0083554P.	PR	25-AUG-1999;	99US-00380142.
PR	29-APR-1998;	98US-0083558P.	PR	29-OCT-1999;	99US-0162506P.
PR	29-APR-1998;	98US-0083559P.	PR	30-NOV-1999;	99WO-US028313.
PR	30-APR-1998;	98US-0083742P.	PR	02-DEC-1999;	99WO-US028551.
PR	05-MAY-1998;	98US-0084366P.	PR	02-DEC-1999;	99WO-US028565.
PR	06-MAY-1998;	98US-0084411P.	PR	16-DEC-1999;	99WO-US030095.
PR	06-MAY-1998;	98US-0084441P.	PR	30-DEC-1999;	99WO-US031243.
PR	07-MAY-1998;	98US-0084598P.	PR	05-JAN-2000;	99WO-US031274.
PR	07-MAY-1998;	98US-0084600P.	PR	06-JAN-2000;	2000WO-US000219.
PR	07-MAY-1998;	98US-0084627P.	PR	06-JAN-2000;	2000WO-US000376.
PR	07-MAY-1998;	98US-0084637P.	PR	11-FEB-2000;	2000WO-US000376.
PR	07-MAY-1998;	98US-0084643P.	PR	18-FEB-2000;	2000WO-US004341.
PR	07-MAY-1998;	98US-0084644P.	PR	24-FEB-2000;	2000WO-US005004.
PR	13-MAY-1998;	98US-0085323P.	PR	10-MAR-2000;	2000WO-US005841.
PR	13-MAY-1998;	98US-0085338P.	PR	21-MAR-2000;	2000WO-US006319.
PR	13-MAY-1998;	98US-0085339P.	PR	30-MAR-2000;	2000WO-US007532.
PR	15-MAY-1998;	98US-0085573P.	PR	17-MAY-2000;	2000WO-US008439.
PR	15-MAY-1998;	98US-0085579P.	PR	22-MAY-2000;	2000WO-US013705.
PR	15-MAY-1998;	98US-0085580P.	PR	30-MAY-2000;	2000WO-US014941.
PR	15-MAY-1998;	98US-0085689P.	PR	02-JUN-2000;	2000WO-US015264.
PR	15-MAY-1998;	98US-0085697P.	PR	28-JUL-2000;	2000WO-US020710.
PR	15-MAY-1998;	98US-0085700P.	PR	24-AUG-2000;	2000WO-US023328.
PR	18-MAY-1998;	98US-0085704P.	PR	08-NOV-2000;	2000US-00709238.
PR	22-MAY-1998;	98US-0086023P.	PR	01-DEC-2000;	2000WO-US032678.
PR	22-MAY-1998;	98US-0086392P.	PR	20-DEC-2000;	2000US-00747259.
PR	22-MAY-1998;	98US-0086414P.	PR	28-FEB-2001;	2000WO-US034956.
PR	22-MAY-1998;	98US-0086430P.	PR	22-MAR-2001;	2001WO-US006520.
PR	28-MAY-1998;	98US-0087098P.	PR	22-MAR-2001;	2001US-00816744.
PR	28-MAY-1998;	98US-0087106P.	PR	22-MAR-2001;	2001US-00816920.
PR	26-JUN-1998;	98US-00105413.	PR	10-MAY-2001;	2001WO-US009552.
PR	26-JUN-1998;	98US-0090863P.	PR	10-MAY-2001;	2001US-00854208.
PR	01-JUL-1998;	98US-0091010P.	PR	25-MAY-2001;	2001WO-US054280.
PR	30-JUL-1998;	98US-0091359P.	PR	01-JUN-2001;	2001US-00872035.
PR	11-SEP-1998;	98US-0094651P.	PR	05-JUN-2001;	2001WO-US017800.
PR	07-OCT-1998;	98US-0100038P.	PR	14-JUN-2001;	2001US-00874503.
PR	02-NOV-1998;	98WO-US021141.	PR	19-JUN-2001;	2001US-00886342.
PR	06-NOV-1998;	98US-00187368.	PR	20-JUN-2001;	2001WO-US019692.
PR	20-NOV-1998;	98US-0109304P.	PR	29-JUN-2001;	2001WO-US021066.
PR	20-NOV-1998;	98WO-US024855.	PR	09-JUL-2001;	2001WO-US021735.
PR	22-DEC-1998;	98US-00202054.	PR	30-JUL-2001;	2001US-00918595.
PR	22-DEC-1998;	98US-00218517.	XX	(GETH) GENENTECH INC.	
PR	22-DEC-1998;	98US-0113296P.	PA		
PR	23-DEC-1998;	98US-0113621P.	XX		
PR	05-JAN-1999;	99WO-US000106.	PI	Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL;	
PR	08-MAR-1999;	99WO-US005028.		Ferrara N, Filvaroff E, Fong S, Gerber H, Gerritsen ME;	
PR	10-MAR-1999;	99US-00265686.			
PR	10-MAR-1999;	99WO-US005190.			

Qy	55	ASGOPPTIRWLNGQPLSMVPPDPHLLPDGTLILLQPPARGHADGQALSTDLGVYTC	114
Db	33	ASGOPPTIRWLNGQPLSMVPPDPHLLPDGTLILLQPPARGHADGQALSTDLGVYTC	92
Qy	115	EASNRLGTAVSRGARSVAVLREDFQIQPRDMVAVGEQFTLECGPPWGHPEPTVSWKXD	174
Db	93	EASNRLGTAVSRGARSVAVLREDFQIQPRDMVAVGEQFTLECGPPWGHPEPTVSWKXD	152
Qy	175	GKPLALQPGHRTVSGGSLMARAEKSDE	202
Db	153	GKPLALQPGHRTVSGGSLMARAEKSDE	180
RESULT 7			
ABU72224			
ID	ABU72224 standard; protein; 985 AA.		
XX			
AC	ABU72224;		
XX			
DT	16-JUN-2003 (first entry)		
XX			
DE	Novel human secreted and transmembrane protein PRO860.		
XX			
KW	Human; secreted and transmembrane protein; PRO; antiinflammatory;		
KW	antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;		
KW	antidiabetic; gene therapy; inflammatory disease; organ failure;		
KW	atherosclerosis; cardiac injury; infertility; birth defect;		
KW	premature aging; AIDS; cancer; diabetic complication; chromosome mapping;		
KW	Gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor;		
KW	tissue typing.		
XX			
OS	Homo sapiens.		
XX			
PN	US2002192706-A1.		
XX			
PD	19-DEC-2002.		
XX			
PF	24-OCT-2001; 2001US-00999832.		
XX			
PR	17-OCT-1997; 97US-0062250P.		
PR	03-NOV-1997; 97US-0064249P.		
PR	13-NOV-1997; 97US-0065311P.		
PR	21-NOV-1997; 97US-0066364P.		
PR	10-MAR-1998; 98US-0077450P.		
PR	11-MAR-1998; 98US-0077632P.		
PR	11-MAR-1998; 98US-0077641P.		
PR	11-MAR-1998; 98US-0077649P.		
PR	12-MAR-1998; 98US-0077791P.		
PR	13-MAR-1998; 98US-0078004P.		
PR	17-MAR-1998; 98US-00040220.		
PR	20-MAR-1998; 98US-0078886P.		
PR	20-MAR-1998; 98US-0078910P.		
PR	20-MAR-1998; 98US-0078936P.		
PR	20-MAR-1998; 98US-0078939P.		
PR	25-MAR-1998; 98US-0079294P.		
PR	26-MAR-1998; 98US-0079656P.		
PR	27-MAR-1998; 98US-0079663P.		
PR	27-MAR-1998; 98US-0079664P.		
PR	27-MAR-1998; 98US-0079689P.		
PR	27-MAR-1998; 98US-0079728P.		
PR	27-MAR-1998; 98US-0079786P.		
PR	30-MAR-1998; 98US-0079920P.		
PR	30-MAR-1998; 98US-0079923P.		
PR	31-MAR-1998; 98US-0080105P.		
PR	31-MAR-1998; 98US-0080107P.		
PR	31-MAR-1998; 98US-0080165P.		
PR	31-MAR-1998; 98US-0080194P.		
PR	01-APR-1998; 98US-0080327P.		
PR	01-APR-1998; 98US-0080328P.		
PR	01-APR-1998; 98US-0080333P.		
PR	01-APR-1998; 98US-0080334P.		
PR	08-APR-1998; 98US-0081049P.		
PR	08-APR-1998; 98US-0081070P.		
PR	08-APR-1998; 98US-0081071P.		
PR	09-APR-1998; 98US-0081195P.		
PR	09-APR-1998; 98US-0081203P.		
PR	09-APR-1998; 98US-0081229P.		
PR	15-APR-1998; 98US-0081817P.		
PR	15-APR-1998; 98US-0081819P.		
PR	15-APR-1998; 98US-0081838P.		
PR	15-APR-1998; 98US-0081952P.		
PR	15-APR-1998; 98US-0081955P.		
PR	21-APR-1998; 98US-0082568P.		
PR	21-APR-1998; 98US-0082569P.		
PR	22-APR-1998; 98US-0082700P.		
PR	22-APR-1998; 98US-0082704P.		
PR	22-APR-1998; 98US-0082797P.		
PR	22-APR-1998; 98US-0082804P.		
PR	23-APR-1998; 98US-0082796P.		
PR	07-OCT-1998; 98WO-US021141.		
PR	20-NOV-1998; 98WO-US024855.		
PR	05-JAN-1999; 99WO-US000106.		
PR	08-MAR-1999; 99WO-US005028.		
PR	10-MAR-1999; 99WO-US005190.		
PR	14-MAY-1999; 99WO-US010733.		
PR	02-JUN-1999; 99WO-US012252.		
PR	30-NOV-1999; 99WO-US028313.		
PR	02-DEC-1999; 99WO-US028551.		
PR	16-DEC-1999; 99WO-US028565.		
PR	30-DEC-1999; 99WO-US030095.		
PR	30-DEC-1999; 99WO-US031243.		
PR	30-DEC-1999; 99WO-US031274.		
PR	03-JAN-2000; 2000WO-US000219.		
PR	06-JAN-2000; 2000WO-US000277.		
PR	11-FEB-2000; 2000WO-US000376.		
PR	18-FEB-2000; 2000WO-US003565.		
PR	24-FEB-2000; 2000WO-US004341.		
PR	02-MAR-2000; 2000WO-US005004.		
PR	10-MAR-2000; 2000WO-US005841.		
PR	21-MAR-2000; 2000WO-US007532.		
PR	30-MAR-2000; 2000WO-US008439.		
PR	17-MAY-2000; 2000WO-US013705.		
PR	22-MAY-2000; 2000WO-US014042.		
PR	30-MAY-2000; 2000WO-US014941.		
PR	02-JUN-2000; 2000WO-US015264.		
PR	28-JUL-2000; 2000WO-US020710.		
PR	24-AUG-2000; 2000WO-US023328.		
PR	01-DEC-2000; 2000WO-US032678.		
PR	20-DEC-2000; 2000WO-US034956.		
PR	28-FEB-2001; 2001WO-US006520.		
PR	22-MAR-2001; 2001WO-US009552.		
PR	25-MAY-2001; 2001WO-US017092.		
PR	01-JUN-2001; 2001WO-US017800.		
PR	20-JUN-2001; 2001WO-US019692.		
PR	29-JUN-2001; 2001WO-US021066.		
PR	09-JUL-2001; 2001WO-US021735.		
XX			
PA	(GETH) GENENTECH INC.		
XX			
PI	Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;		
PI	Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;		
PI	Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;		
PI	Klavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;		
PI	Stewart TA, Tumas D, Williams PM, Wood WI;		
XX			
DR	WPI; 2003-328860/31.		
DR	N-PSDB; ACA63637.		
XX			
PT	New secreted and transmembrane nucleic acids and polypeptides, designated		
PT	as PRO, useful for treating inflammation, organ failure, atherosclerosis,		
PT	cardiac injury, infertility, birth defects, premature aging, AIDS, or		
PT	cancer.		
XX			
PS	Claim 12; Fig 77; 453pp; English.		
XX			

CC The invention describes an isolated nucleic acid (I) comprising, or which
 CC is at least 80 % sequence identity to, or the full-length coding sequence
 CC of, any of 118 300-2100 nucleotide sequences, which encodes its
 CC corresponding PRO polypeptide selected from 118 100-700 amino acid
 CC sequences, all given in the specification. The nucleic acids and
 CC polypeptides are useful for treating inflammatory diseases, organ
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
 CC premature aging, AIDS, cancer, or diabetic complications. The nucleic
 CC acids are useful as hybridisation probes, in chromosome and gene mapping,
 CC and in generating antisense RNA or DNA. The polypeptides are useful as
 CC pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful
 CC in tissue typing. This is the amino acid sequence of a novel human
 CC secreted and transmembrane PRO polypeptide
 XX
 SQ Sequence 985 AA;

Query Match 48.8%; Score 148; DB 6; Length 985;
 Best Local Similarity 100.0%; Pred. No. 3.5e-130;
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 55 ASGGPPPTIRLLNGQPLSMVPPDPHLLPDGTLTLLQPPARGHAHDGQALSTDLGYTC 114
 DB 33 ASGGPPPTIRLLNGQPLSMVPPDPHLLPDGTLTLLQPPARGHAHDGQALSTDLGYTC 92
 QY 115 EASRLGTAVSRGRLSVAVLRDPQIQPRDMVAVGGEQFTLECGPPWGHPEPTVSWKWD 174
 DB 93 EASRLGTAVSRGRLSVAVLRDPQIQPRDMVAVGGEQFTLECGPPWGHPEPTVSWKWD 152
 QY 175 GKPLALQPGRTVSGSLLMARAEKSD 202
 DB 153 GKPLALQPGRTVSGSLLMARAEKSD 180

RESULT 8
 ABUS4904
 ID ABUS4904 standard; protein; 985 AA.
 XX
 AC ABUS4904;
 XX
 DT 12-AUG-2003 (first entry)
 XX
 DE Human secreted and transmembrane polypeptide PRO860.
 XX
 KW Human; thrombolytic agent; interferon; interleukin; cytokine;
 KW erythropoietin; colony stimulating factor; cancer; colorectal carcinoma;
 KW apoptosis related condition; AIDS; ankyrotrophic lateral sclerosis;
 KW inflammatory disease; asthma; atherosclerosis; neurodegenerative disease;
 KW gastrointestinal disorder; Alzheimer's disease; Parkinson's disease;
 KW hypertension; myocardial ischemia; kidney disease; carcinogenesis;
 KW glomerulonephritis; lung disease; pulmonary hypertension; preclampsia;
 KW bronchial asthma; gastric ulcer; renal failure; cardiovascular disease;
 KW inflammatory bowel disease; reproductive disorder; premature labour.
 XX
 OS Homo sapiens.
 XX
 PN US2002177553-A1.
 XX
 PD 28-NOV-2002.
 XX
 PF 15-OCT-2001; 2001US-00978192.
 XX
 PR 17-OCT-1997; 97US-0062250P.
 PR 03-NOV-1997; 97US-0064249P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 10-MAR-1998; 98US-0077450P.
 PR 11-MAR-1998; 98US-0077632P.
 PR 11-MAR-1998; 98US-0077641P.
 PR 11-MAR-1998; 98US-0077649P.
 PR 12-MAR-1998; 98US-0077791P.
 PR 13-MAR-1998; 98US-0078004P.
 PR 17-MAR-1998; 98US-0080402P.
 PR 20-MAR-1998; 98US-0078886P.

PR 20-MAR-1998; 98US-0078910P.
 PR 20-MAR-1998; 98US-0078936P.
 PR 25-MAR-1998; 98US-0078939P.
 PR 26-MAR-1998; 98US-0079294P.
 PR 27-MAR-1998; 98US-0079656P.
 PR 27-MAR-1998; 98US-0079663P.
 PR 27-MAR-1998; 98US-0079664P.
 PR 27-MAR-1998; 98US-0079689P.
 PR 27-MAR-1998; 98US-0079728P.
 PR 30-MAR-1998; 98US-0079786P.
 PR 30-MAR-1998; 98US-0079920P.
 PR 30-MAR-1998; 98US-0079923P.
 PR 26-JUN-1998; 98US-00105413.
 PR 07-OCT-1998; 98US-00158978.
 PR 07-OCT-1998; 98WO-US021141.
 PR 02-NOV-1998; 98US-00154216.
 PR 06-NOV-1998; 98US-00157368.
 PR 20-NOV-1998; 98WO-US024855.
 PR 22-DEC-1998; 98US-00202054.
 PR 05-JAN-1999; 99WO-US000106.
 PR 05-MAR-1999; 99US-00254465.
 PR 08-MAR-1999; 99WO-US005028.
 PR 10-MAR-1999; 99US-00265686.
 PR 10-MAR-1999; 99WO-US005190.
 PR 12-MAR-1999; 99US-00267213.
 PR 12-APR-1999; 99US-00284231.
 PR 14-MAY-1999; 99US-00311832.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 25-AUG-1999; 99US-00380137.
 PR 25-AUG-1999; 99US-00380138.
 PR 25-AUG-1999; 99US-00380142.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 11-FEB-2000; 2000WO-US000376.
 PR 18-FEB-2000; 2000WO-US003565.
 PR 24-FEB-2000; 2000WO-US004341.
 PR 02-MAR-2000; 2000WO-US005004.
 PR 10-MAR-2000; 2000WO-US005841.
 PR 21-MAR-2000; 2000WO-US006319.
 PR 30-MAR-2000; 2000WO-US007532.
 PR 17-MAY-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US013705.
 PR 30-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US014941.
 PR 28-JUL-2000; 2000WO-US015264.
 PR 24-AUG-2000; 2000WO-US020710.
 PR 08-NOV-2000; 2000WO-US023328.
 PR 27-NOV-2000; 2000US-00723749.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 22-MAR-2001; 2001US-00816744.
 PR 22-MAR-2001; 2001US-00816920.
 PR 22-MAR-2001; 2001WO-US009552.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.

PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 30-JUL-2001; 2001US-00918585.
 XX (GETH) GENENTECH INC.
 XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
 PI Stewart TA, Tumas D, Williams PM, Wood WI;
 XX WPI; 2003-328499/31.
 DR N-PSDB; ACAV1801.
 DR
 XX New isolated PRO polypeptides e.g. PRO213, PRO274 and PRO300, for use as
 PT pharmaceuticals, diagnostics, biosensors and bioreactors, for identifying
 PT modulators of receptor-ligand interactions.
 XX
 PS Claim 12; SEQ ID NO 211; 55pp; English.
 XX
 CC The invention relates to an isolated secreted and transmembrane
 CC polypeptide, designated as PRO polypeptide. The PRO polypeptide is useful
 CC in PRO polypeptide detection methods. The PRO polypeptide is useful for
 CC linking a bioactive molecule to a cell. The PRO polypeptide or an
 CC antibody against it is useful for modulating a biological activity of a
 CC cell. The PRO polypeptide is useful in industrial applications including
 CC pharmaceuticals, diagnostics, biosensors and bioreactors. The PRO
 CC polypeptide is also useful as a thrombolytic agent, interferon,
 CC interleukin, erythropoietin, colony stimulating factor and other
 CC cytokines. The PRO polypeptide is useful for treating disease such as
 CC cancer e.g. colorectal carcinoma, apoptosis related conditions e.g. AIDS,
 CC amyotrophic lateral sclerosis; inflammatory disease e.g. asthma,
 CC atherosclerosis; neurodegenerative disease e.g. Alzheimer's disease,
 CC Parkinson's disease; cardiovascular disease e.g. hypertension and
 CC myocardial ischaemia; kidney disease e.g. renal failure and
 CC glomerulonephritis; lung disease e.g. pulmonary hypertension, bronchial
 CC asthma; gastrointestinal disorders e.g. gastric ulcer and inflammatory
 CC bowel disease; reproductive disorders e.g. premature labour and
 CC preclampsia; carcinogenesis. The present sequence represents the amino
 CC acid sequence of a PRO polypeptide of the invention. Note: The sequence
 CC data for this patent did not form part of the printed specification but
 CC was obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20020177553
 XX
 SQ Sequence 985 AA;
 Query Match 48.8%; Score 148; DB 6; Length 985;
 Best Local Similarity 100.0%; Pred. No. 3.5e-130;
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 55 ASGGPPPTIRLLNGQPLSMVPPPHLLPDGTLILLQPPARGHAHQALSTDLGVYTC 114
 Db |||||
 Qy 33 ASGGPPPTIRLLNGQPLSMVPPPHLLPDGTLILLQPPARGHAHQALSTDLGVYTC 92
 Db |||||
 Qy 115 EASNRLGTAVSRGARLSVAVLRDFQIQPRDMVAVVGGEQFTLECGPPWGHPEPTVSWWKD 174
 Db |||||
 Qy 93 EASNRLGTAVSRGARLSVAVLRDFQIQPRDMVAVVGGEQFTLECGPPWGHPEPTVSWWKD 152
 Db |||||
 Qy 175 GKPLALQGRHTVSGSLMARAEKSD 202
 Db |||||
 Qy 153 GKPLALQGRHTVSGSLMARAEKSD 180
 Db |||||
 RESULT 9
 ABU61102
 ID ABU61102 standard; protein; 985 AA.
 XX
 AC ABU61102;
 XX
 DT 08-MAY-2003 (first entry)
 XX
 DE Human PRO860 polypeptide.

XX Human; PRO polypeptide; secreted and transmembrane protein;
 KW immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;
 KW cardiac insufficiency; nervous system disorder; kidney disorder;
 KW bone disorder; cartilage disorder; arthritis; tumour; wound healing;
 KW genetic disorder; cytostatic; antidiabetic; antiinflammatory;
 KW antiarthritic; anti-tumour; vulnery; antianaemic; dermatological;
 KW cardiant.
 XX Homo sapiens.
 XX US2002169284-A1.
 XX
 PD 14-NOV-2002.
 XX
 PF 16-OCT-2001; 2001US-00978697.
 XX
 PR 26-MAY-1981; 81US-00267213.
 PR 17-OCT-1997; 97US-0062250P.
 PR 03-NOV-1997; 97US-0064249P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 21-NOV-1997; 97US-0065364P.
 PR 10-MAR-1998; 98US-0077450P.
 PR 11-MAR-1998; 98US-0077632P.
 PR 11-MAR-1998; 98US-0077641P.
 PR 11-MAR-1998; 98US-0077649P.
 PR 12-MAR-1998; 98US-0077791P.
 PR 13-MAR-1998; 98US-0078004P.
 PR 17-MAR-1998; 98US-00040220.
 PR 20-MAR-1998; 98US-0078886P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 20-MAR-1998; 98US-0078936P.
 PR 20-MAR-1998; 98US-0078939P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 26-MAR-1998; 98US-0079656P.
 PR 27-MAR-1998; 98US-0079663P.
 PR 27-MAR-1998; 98US-0079664P.
 PR 27-MAR-1998; 98US-0079689P.
 PR 27-MAR-1998; 98US-0079728P.
 PR 27-MAR-1998; 98US-0079786P.
 PR 30-MAR-1998; 98US-0079920P.
 PR 30-MAR-1998; 98US-0079923P.
 PR 26-JUN-1998; 98US-00105413.
 PR 07-OCT-1998; 98US-00188978.
 PR 07-OCT-1998; 98WO-US021141.
 PR 02-NOV-1998; 98US-00184216.
 PR 06-NOV-1998; 98US-00187368.
 PR 20-NOV-1998; 98WO-US024855.
 PR 07-DEC-1998; 98US-00202054.
 PR 22-DEC-1998; 98US-00218517.
 PR 05-JAN-1999; 99WO-US000106.
 PR 05-MAR-1999; 99US-00254465.
 PR 08-MAR-1999; 99US-00254465.
 PR 10-MAR-1999; 99US-00265686.
 PR 10-MAR-1999; 99WO-US005190.
 PR 12-APR-1999; 99US-00284291.
 PR 14-MAY-1999; 99US-00311832.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 25-AUG-1999; 99US-00380137.
 PR 25-AUG-1999; 99US-00380138.
 PR 25-AUG-1999; 99US-00380142.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 11-FEB-2000; 2000WO-US000376.
 PR 18-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.

PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 10-MAY-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 14-JUN-2001; 2001US-00874503.
PR 05-JUN-2001; 2001US-00886236.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Klijavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams FM, Wood WI;
XX
XX WPI; 2003-288163/28.
DR N-PSDB; ABX92441.
XX
XX Novel secreted and transmembrane polypeptides and polynucleotides
PT encoding them useful for treating cancer, kidney diseases, bone,
PT cartilage disorders and immune deficiencies.
XX
XX Claim 12; Fig 77; 459pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for
CC identifying agonists or antagonists. The bioactive molecule maybe a
CC toxin, radiolabel or antibody, and causes apoptosis or death of the cell.
CC The PRO polypeptides are useful for treating immune disorders, diabetes
CC or hyper- or hypo-insulinaemia, cardiac insufficiency, nervous system
CC disorders, kidney disorders, bone and cartilage disorders or arthritis,
CC tumours, and wound healing. The polynucleotide sequences encoding PRO
CC polypeptides are useful as hybridisation probes, in chromosome and gene
CC mapping, in the generation of antisense RNA and DNA, in the preparation
CC of PRO polypeptides, for generating transgenic animals or knockout
CC animals, for the genetic analysis of individuals with genetic disorders,
CC and in gene therapy. ABU61071-ABU61164 represent the human PRO
CC polypeptides of the invention. Note: The sequence data for this patent
CC was obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/peipsdbEntry.html
XX
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QY 175 GKPLALQPGRHVTSGSLLMARAEXSDE 202
Db 153 GKPLALQPGRHVTSGSLLMARAEXSDE 180
RESULT 10
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XX ABU80371;
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XX 24-JUN-2003 (first entry)
XX
XX Human secreted/transmembrane protein PRO860.
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XX Human; secreted protein; transmembrane protein; PRO; malignancy; cancer;
KW ovarian cancer; colorectal cancer; sarcoma; leukaemia; lymphoma;
KW inflammatory disease; necrosis; atherosclerosis; infertility;
KW premature aging; psoriasis; inflammatory disease; renal disease;
KW arthritis; immune-mediated alopecia; stroke; encephalitis; hepatitis;
KW multiple sclerosis; gene therapy.
XX
XX Homo sapiens.
OS
XX US2003004102-A1.
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XX 02-JAN-2003.
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XX 15-OCT-2001; 2001US-00978189.
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PR 11-MAR-1998; 98US-0077632P.
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PR 07-OCT-1998; 98WO-US021141.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98WO-US024855.
PR 07-DEC-1998; 98US-00202054.

OS Homo sapiens.
XX US2003050241-Al.
XX 13-MAR-2003.
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PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
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PR 02-MAR-2000; 2000WO-US005841.
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PR 05-JAN-2000; 2000US-00000219.

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PR 22-MAR-2001; 2001WO-US009552.
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PR 21-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
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PA (GETH) GENENTECH INC.
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PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
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Query Match 48.8%; Score 148; DB 6; Length 985;
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QY 175 GKPLALQPGRTVSGGSLLMARAEKSDE 202
Db 153 GKPLALQPGRTVSGGSLLMARAEKSDE 180
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XX 27-AUG-2003 (first entry)
DE Novel human secreted and transmembrane polypeptide #32.
XX Human; secreted and transmembrane protein; PRO; viral infection;
KW tumour growth; retinal disorder; injury; sight loss;
KW retinitis pigmentosum; age-related macular degeneration;
KW sport-related joint problem; articular cartilage defect; osteoarthritis;

KW rheumatoid arthritis; wound healing; obesity; diabetes; insulinaemia;
KW kidney disorder; mesangial cell function; Berger disease; nephropathy;
KW celiac disease; dermatitis; Crohn disease; neuropathy;
KW cardiac insufficiency disorder; peripheral neuropathy;
KW diabetic peripheral neuropathy; autonomic neuropathy;
KW reduced motility of the gastrointestinal tract;
KW atony of the urinary bladder; post polio syndrome; Krabbe's disease;
KW Charcot-Marie-Tooth disease; Fabry's disease; Tangier disease;
KW Refsum's disease.
XX
XX Homo sapiens.
XX
XX US2003049633-A1.
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XX 13-MAR-2003.
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PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083392P.
PR 29-APR-1998; 98US-0083485P.
PR 29-APR-1998; 98US-0083496P.

PR	29-APR-1998;	98US-0083499P.
PR	29-APR-1998;	98US-0083500P.
PR	29-APR-1998;	98US-0083545P.
PR	29-APR-1998;	98US-0083554P.
PR	29-APR-1998;	98US-0083558P.
PR	29-APR-1998;	98US-0083559P.
PR	30-APR-1998;	98US-0083742P.
PR	05-MAY-1998;	98US-0084366P.
PR	06-MAY-1998;	98US-0084414P.
PR	07-MAY-1998;	98US-0084598P.
PR	07-MAY-1998;	98US-0084600P.
PR	07-MAY-1998;	98US-0084627P.
PR	07-MAY-1998;	98US-0084637P.
PR	07-MAY-1998;	98US-0084639P.
PR	07-MAY-1998;	98US-0084640P.
PR	07-MAY-1998;	98US-0084643P.
PR	13-MAY-1998;	98US-0085323P.
PR	13-MAY-1998;	98US-0085338P.
PR	13-MAY-1998;	98US-0085339P.
PR	15-MAY-1998;	98US-0085573P.
PR	15-MAY-1998;	98US-0085579P.
PR	15-MAY-1998;	98US-0085580P.
PR	15-MAY-1998;	98US-0085582P.
PR	15-MAY-1998;	98US-0085689P.
PR	15-MAY-1998;	98US-0085697P.
PR	15-MAY-1998;	98US-0085700P.
PR	15-MAY-1998;	98US-0085704P.
PR	18-MAY-1998;	98US-0086023P.
PR	22-MAY-1998;	98US-0086392P.
PR	22-MAY-1998;	98US-0086414P.
PR	22-MAY-1998;	98US-0086430P.
PR	22-MAY-1998;	98US-0086486P.
PR	28-MAY-1998;	98US-0087098P.
PR	28-MAY-1998;	98US-0087106P.
PR	28-MAY-1998;	98US-0087208P.
PR	26-JUN-1998;	98US-00105413.
PR	26-JUN-1998;	98US-0090863P.
PR	26-JUN-1998;	98US-0091010P.
PR	01-JUL-1998;	98US-0091359P.
PR	30-JUL-1998;	98US-0094651P.
PR	11-SEP-1998;	98US-0100038P.
PR	07-OCT-1998;	98US-00168978.
PR	07-OCT-1998;	98WO-US021141.
PR	02-NOV-1998;	98US-00184216.
PR	06-NOV-1998;	98US-00187368.
PR	20-NOV-1998;	98US-0109304P.
PR	20-NOV-1998;	98WO-US02485S.
PR	07-DEC-1998;	98US-00202054.
PR	22-DEC-1998;	98US-00218517.
PR	23-DEC-1998;	98US-0113296P.
PR	23-DEC-1998;	98US-0113621P.
PR	03-JAN-1999;	98WO-US000106.
PR	03-MAR-1999;	98US-0025446S.
PR	08-MAR-1999;	98WO-US005028.
PR	10-MAR-1999;	98US-00265686.
PR	10-MAR-1999;	98WO-US0005190.
PR	12-MAR-1999;	98US-00267213.
PR	12-MAR-1999;	98US-0123957P.
PR	23-MAR-1999;	98US-0126773P.
PR	12-APR-1999;	98US-00284291.
PR	21-APR-1999;	98US-0130232P.
PR	26-APR-1999;	98US-0131022P.
PR	28-APR-1999;	98US-0131445P.
PR	14-MAY-1999;	98US-00311832.
PR	14-MAY-1999;	98US-0134287P.
PR	14-MAY-1999;	98WO-US010733.
PR	02-JUN-1999;	98WO-US012252.
PR	16-JUN-1999;	98US-0139557P.
PR	23-JUN-1999;	98US-0141037P.
PR	07-JUL-1999;	98US-0142680P.
PR	26-JUL-1999;	98US-0145698P.
PR	28-JUL-1999;	98US-0146222P.
PR	25-AUG-1999;	99US-00380137.
PR	25-AUG-1999;	99US-00380138.
PR	25-AUG-1999;	99US-00380142.
PR	29-OCT-1999;	99US-0162506P.
PR	30-NOV-1999;	99WO-US028313.
PR	02-DEC-1999;	99WO-US028551.
PR	02-DEC-1999;	99WO-US028565.
PR	16-DEC-1999;	99WO-US030095.
PR	30-DEC-1999;	99WO-US031243.
PR	30-DEC-1999;	99WO-US031274.
PR	05-JAN-2000;	2000WO-US000219.
PR	06-JAN-2000;	2000WO-US000277.
PR	06-JAN-2000;	2000WO-US000376.
PR	11-FEB-2000;	2000WO-US003565.
PR	18-FEB-2000;	2000WO-US004341.
PR	24-FEB-2000;	2000WO-US005004.
PR	02-MAR-2000;	2000WO-US005841.
PR	10-MAR-2000;	2000WO-US006319.
PR	21-MAR-2000;	2000WO-US007532.
PR	30-MAR-2000;	2000WO-US008439.
PR	17-MAY-2000;	2000WO-US013705.
PR	22-MAY-2000;	2000WO-US014042.
PR	30-MAY-2000;	2000WO-US014941.
PR	02-JUN-2000;	2000WO-US015264.
PR	28-JUL-2000;	2000WO-US020710.
PR	24-AUG-2000;	2000WO-US023328.
PR	08-NOV-2000;	2000US-00709238.
PR	27-NOV-2000;	2000US-00723749.

Search completed: February 27, 2004, 19:37:31
Job time : 81 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 29, 2004, 22:51:23 ; Search time 455 Seconds

(without alignments)
2829.020 Million cell updates/sec

Title: US-10-047-021-86

Perfect score: 303

Sequence: 1 MGSGGSLGGRGSLPLLLL.....SGRLPREARELGRORNTG 303

Scoring table:

Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Word size: 1

Total number of hits satisfying chosen parameters: 6745146

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-DB=N_Geneseq_29Jan04 -OPMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=EXT -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10047021@cgn 1.1 470 @runat_20022004_154121_4513 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

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1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	300	99.0	1346	2	Aax51721 DNA encod
2	300	99.0	1346	6	Abq92573 Human sec
3	148	48.8	3267	6	Abn59723 Novel hum
4	148	48.8	3715	6	Abk87137 cDNA huma
5	148	48.8	3715	2	Aaz34069 Human PRO
6	148	48.8	3716	3	Aac78502 Human PRO
7	148	48.8	3716	7	ACD42602 Novel hum
8	148	48.8	3716	7	ACA63637 Novel hum

9	148	48.8	3716	7	ACA71801	Aca71801 Human sec
10	148	48.8	3716	7	ABX92441	Abx92441 cDNA enco
11	148	48.8	3716	7	ACA66182	ACA66182 Human cDN
12	148	48.8	3716	8	ADA24749	Ada24749 Novel hum
13	148	48.8	3716	8	ACD29783	AcD29783 Novel hum
14	148	48.8	3716	8	ADA12410	Ada12410 Human cDN
15	148	48.8	3716	8	ACD29198	AcD29198 Novel hum
16	148	48.8	3716	9	ADB73716	AdB73716 Human PRO
17	148	48.8	3716	9	ADB76432	AdB76432 Human PRO
18	148	48.8	3716	9	ADC43858	AdC43858 Human cDN
19	148	48.8	3716	9	ADC61618	AdC61618 Human cDN
20	148	48.8	3716	9	ADC63582	AdC63582 Human cDN
21	148	48.8	3716	9	ADC66682	AdC66682 Human cDN
22	148	48.8	3716	9	ADC68806	AdC68806 Human cDN
23	148	48.8	3716	9	ADC62866	AdC62866 Human cDN
24	148	48.8	3716	9	ADC67931	AdC67931 Human cDN
25	148	48.8	3716	9	ADC41251	AdC41251 Human cDN
26	148	48.8	3716	9	ADC67306	AdC67306 Human cDN
27	148	48.8	3716	9	ADC62242	AdC62242 Human cDN
28	148	48.8	3716	9	ADC41875	AdC41875 Human cDN
29	148	48.8	3716	9	ADE49244	AdE49244 Human cDN
30	148	48.8	3716	9	ADE35298	AdE35298 Human cDN
31	148	48.8	3716	9	ADE16412	AdE16412 Human cDN
32	148	48.8	3716	9	ADD73027	AdD73027 Human cDN
33	148	48.8	3716	9	ADD72385	AdD72385 Human cDN
34	148	48.8	3716	9	ADE17036	AdE17036 Human cDN
35	148	48.8	3716	10	ADE89645	AdE89645 Human cDN
36	148	48.8	3716	10	ADE89645	AdE89645 Human cDN
37	148	48.8	3808	4	AAH01695	AaH01695 Human TAN
38	120	39.6	756	4	AAH08234	AaH08234 Human TAN
39	120	39.6	4262	4	AAH18180	AaH18180 Human cDN
40	120	39.6	4262	5	AAH78073	AaH78073 Nucleotid
41	110	36.3	3042	4	AAH01694	AaH01694 Human TAN
42	40	13.2	232	3	AAZ42889	AaZ42889 Human 5'
43	33	10.9	299	4	AAZ35325	AaZ35325 Human car
44	33	10.9	299	9	ADE45404	AdE45404 Human car
45	30	9.9	1943	8	ACH04142	Ach04142 Human cDN

ALIGNMENTS

RESULT 1

ID AAX51721 standard; DNA; 1346 BP.

XX AC AAX51721;

XX DT 17-JUN-1999 (first entry)

XX DE DNA encoding a human secreted protein.

XX KW Human secreted protein; cancer; immune disorder; infection;

KW inflammatory disorder; skin disorder; tumour; atherosclerosis;

KW restenosis; autoimmune disorder; Alzheimer's disease;

KW peripheral neuropathy; trauma; spinal cord injury; allergy;

KW hematopoietic disorder; skeletal disorder; neurological disorder;

KW arthritic disorder; asthma; immunodeficiency disease; AIDS;

KW transplant rejection; ss.

XX OS Homo sapiens.

XX PN WO9911293-A1.

XX PD 11-MAR-1999.

XX PF 03-SEP-1998; 98WO-US018360.

XX PR 05-SEP-1997; 97US-0057626P.

PR 05-SEP-1997; 97US-0057663P.

PR 05-SEP-1997; 97US-0057669P.

PR 12-SEP-1997; 97US-0058666P.

PR 12-SEP-1997; 97US-0058667P.

PR 12-SEP-1997; 97US-0058973P.

PR 12-SEP-1997; 97US-0058974P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Moore PA, Ruben SM, Lafleur DW, Shi Y, Rosen GA, Olsen HS;
 PI Ebner R, Brewer LA;
 XX WPI; 1999-204988/17.
 DR P-PSDB; AAY12934.
 XX New isolated human genes and the secreted polypeptides they encode -
 PT useful for diagnosis and treatment of e.g. neurological disorders,
 PT tumors, immune disorders, inflammation or hematological disorders.
 XX Claim 1; Page 165-166; 215pp; English.
 XX AAX51701-55 encode human secreted proteins. The polynucleotides and their
 CC corresponding secreted polypeptides are useful for preventing, treating
 CC or ameliorating medical conditions, e.g. by protein or gene therapy.
 CC Pathological conditions can also be diagnosed by determining the amount
 CC of the new polypeptides in a sample or by determining the presence of
 CC mutations in the new polynucleotides. Specific uses are described for
 CC each polynucleotide, based on which tissues they are most highly
 CC expressed in, and include developing products for the diagnosis or
 CC treatment of cancer, immune disorders, infection, inflammatory disorders,
 CC skin disorders, tumours, atherosclerosis, restenosis, autoimmune
 CC disorders, Alzheimer's disease, peripheral neuropathies, trauma, spinal
 CC cord injuries, allergy, hematopoietic disorders, skeletal disorders,
 CC neurological disorders, arthritic disorders, asthma, immunodeficiency
 CC diseases, AIDS and transplant rejection. The polypeptides are also useful
 CC for identifying their binding partners
 XX
 SQ Sequence 1346 BP; 318 A; 379 C; 376 G; 267 T; 0 U; 6 Other;

Alignment Scores:
 Pred. No.: 1,76e-263 Length: 1346
 Score: 300.00 Matches: 303
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.01% Indels: 0
 DB: 2 Gaps: 0

US-10-047-021-86 (1-303) x AAX51721 (1-1346)

QY 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20
 Db 31 ATGGGCTCTGGAGAGACAGCTCTGGGGGCGAGGGGTTCCCTGCTGCTGCTGCTG 90
 QY 21 LeuileMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp 40
 Db 91 CTCATCATGGGAGGCGATGGCTCAGAGCTCCCCGGCCCGAGATCTAGTCCACCCCGAGGAC 150
 QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
 Db 151 CAGCTGTTCACAGGCGCTGGCCCTGCCAGGATGAGCTGCCAGCCTCAGGCCAGCCACCT 210
 QY 61 ProThrIleArgTTPLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
 Db 211 CCCACCATCCGCTGGTTGCTGANTGGGAGGCCCTTGAGCATGGTGCCCCAGACCCACAC 270
 QY 81 HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
 Db 271 CACCTCTCGCTGATGGAGCCCTTCTGCTGTACAGGCCCTCCCGGGGACATGCCAC 330
 QY 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120
 Db 331 GATGGCAGGCGCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCACACCGGCTT 390
 QY 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
 Db 391 GGCACGCGAGTCACAGAGGCGCTCGGCTGTCTGTGCTGTCTGCCGGGAGGATTTCCAG 450
 QY 141 IleGlnProArgAspMetValAlaValAlaValGlyGlnPheThrLeuGluCysGlyPro 160

Db 451 ATCCAGGCTCGGACATGGTGGCTGTGGTGGTGGAGCAGTTTACTCTGGAATGTGGCGG 510
 QY 161 ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeu 180
 Db 511 CCTGGGGCCACCCAGAGCCACAGTCTCTGTGTGAAAGATGGGAAACCCCTGGCCCTC 570
 QY 181 GlnProGlyValGlyHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSer 200
 Db 571 GAGCCCGGAGGACACACAGTGTCCGGGGGTCCCTGCTGATGGCAGAGCAGAGAGAGT 630
 QY 201 AspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAla 220
 Db 631 GACGAANGGACCTACATGTGTGTGGCCACCAACAGCGCAGGACACAGGAGAGCCGCCA 690
 QY 221 AlaArgValSerIleGlnGlnProGlnAspTyrThrGluProValGluLeuAlaVal 240
 Db 691 GCCCGGTTTCCATCCAGAGCCCGAGGACTACCGAGGCTGTGGAGCTTCTGGCTGTG 750
 QY 241 ArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysPro 260
 Db 751 CGAATTTCAGCTGGAATGTGACACTCTGAACCGGATCTCTGCAGARGGCCCAAGCCT 810
 QY 261 ArgProAlaValTrpLeu***TrpLysValSerGlyPro***ArgLeuProAsnLeuThr 280
 Db 811 AGACCGCGGTGTGGCTCARTGGAAAGTCACTGGCGCCCTNTGGCGCTGCCCAATCTTACA 870
 QY 281 ArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArgArg 300
 Db 871 CGGCTTGTTCAGGACCCAGACTGCCCGGGAGGCCAGGAGCTCCGTGGGCGAGGAGG 930
 QY 301 AsnThrGly 303
 Db 931 AACACAGGA 939

RESULT 2
 ABQ92573
 ID ABQ92573 standard; cDNA; 1346 BP.
 XX AC ABQ92573;
 XX DT 12-NOV-2002 (first entry)
 XX DE Human secreted protein encoding cDNA SEQ ID NO 31.
 XX KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
 KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
 KW antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
 KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
 KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
 KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine;
 XX gene; ss.
 XX OS Homo sapiens.
 XX WC200257420-A2.
 XX PD 25-JUL-2002.
 XX PF 17-JAN-2002; 2002WO-US001109.
 XX PR 18-JAN-2001; 2001US-0262066P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Moore PA, Ruben SM, Lafleur DW, Shi Y, Rosen CA, Olsen H;
 PI Ebner R, Brewer LA;
 XX WPI; 2002-599716/64.
 DR P-PSDB; ABP62033.
 XX New polynucleotides and polypeptides useful for diagnosing, prognosing,

PT treating or preventing e.g. neurodegenerative, central nervous system,
 PT autoimmune, respiratory, reproductive, or inflammatory diseases or
 XX disorders.

Claim 1; Page 713-714; 785pp; English.

XX The invention relates to novel genes (ABQ2553-ABQ2607) and proteins
 CC (ABP62013-ABP62153) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 XX infections

SQ Sequence 1346 BP; 318 A; 379 C; 376 G; 267 T; 0 U; 6 Other;

Alignment Scores:

Pred. No.: 1.76e-263 Length: 1346
 Score: 300.00 Matches: 303
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.01% Indels: 0
 DB: 6 Gaps: 0

US-10-047-021-86 (1-303) x ABQ92573 (1-1346)

Qy	1	MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu	20
Db	31	ATGGGCTCTGGAGGAGACACGCTCTGGGGGGAGGGTTCCTGCTCTGCTGCTGCTG	90
Qy	21	LeuileMetGlyGlyMetAlaGlnAspSerProProGlnileLeuValHisProGlnAsp	40
Db	91	CTCATCTGGAGGATGGCTCAGGACTCCCGCCCCCAGATCTTAGTCCACCCCGAGGAC	150
Qy	41	GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro	60
Db	151	CAGCTGTTCAGGGCCCTGGCCCTGCCAGGATGAGTGTCCGAGCCTCAGGCCACGACCT	210
Qy	61	ProThrileArgTTPLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis	80
Db	211	CCACCATCCCTGTTGCTGATGGGAGCCCTGAGCATGGTCCCGCCGAGCCACAC	270
Qy	81	HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis	100
Db	271	CACCTCTGCTGATGGACCCCTTCTGCTGCTACAGCCCTCTGCGGGGACATGCCAC	330
Qy	101	AspGlyGlnAlaLeuSerThrAspLeuGlyValTyThrCysGluAlaSerAsnArgLeu	120
Db	331	GATGCCAGGGCCCTGTCCACAGACTGGGTGTCTACACATGTGAGGCCAGCACCCGCTT	390
Qy	121	GlyThrAlaValSerAGlyValaArgLeuSerValAlaValLeuArgGluAspPheGln	140
Db	391	GGCAGGCGAGTCAGAGGGCTCGGCTGCTCTGCTGCTCTGCTGCTGCTGCTGCTGCT	450
Qy	141	IleGlnProArgAspMetValAlaValGlyGlnGlnPheThrLeuGluCysGlyPro	160
Db	451	ATCCAGGCTCCGGGACATGGTGGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	510
Qy	161	ProTrpGlyHisProGluProThrValSerTrpTrpIysAspGlyLysProLeuAlaLeu	180
Db	511	CCCTGGGGCCACCCAGAGCCACAGTCTCATGTGGTGGTGGTGGTGGTGGTGGTGGTGG	570
Qy	181	GlnProGlyArgHisThrValSerGlyLysSerLeuLeuMetAlaArgAlaGluLysSer	200
Db	571	CAGCCCGAGGACACACAGTGTCCGGGGGGTCCCTGCTGTGATGGCAAGACAGAGAGT	630

Qy	201	AspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAla	220
Db	631	GACGAANGGACCTACATGTGTGGCCACCAACAGCGCAGGACACAGGAGAGCGCGCA	690
Qy	221	AlaArgValSerIleGlnGluProGlnAspTyThrGluProValGluLeuAlaVal	240
Db	691	GCCCGGGTTTCATCCAGAGGCCACGAGCTACACGGAGCCTGTGGAGCTTCTGGCTGTG	750
Qy	241	ArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGlyProIysPro	260
Db	751	CGAATTCAGCTGGAATAATGTGACACTCTGAACCCGGATCTGCAGARGGCCCAAGCCT	810
Qy	261	ArgProAlaValTrrLeu***TrpIysValSerGlyPro***ArgLeuProAsnLeuThr	280
Db	811	AGACCGGGGTGTGGCTCARTGGNARTCAGTGGCCCTNTGGCCTGCCCAATCTTACA	870
Qy	281	ArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArgArg	300
Db	871	CGGCTTGTTCAGGACCCAGACTGCCCGGGAGGCCAGGAGTCCGTGGGCGAGGAGG	930
Qy	301	AsnThrGly 303	
Db	931	AACACAGGA 939	

RESULT 3

ABN59723
 ID ABN59723 standard; cDNA; 3267 BP.

AC ABN59723;

DT 28-JUN-2002 (first entry)

XX Novel human coding sequence SEQ ID NO: 134.

XX Human; antianemic; vulnerary; antiinflammatory; immunomodulator;
 KW antifertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
 KW neuroprotective; antiparkinsonian; protein therapy; EST;
 KW expressed sequence tag; gene; ss.

OS Homo sapiens.

XX WO200222660-A2.

XX 21-MAR-2002.

XX 10-SEP-2001; 2001WO-US026015.

XX 11-SEP-2000; 2000US-00659671.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;

XX WPI; 2002-292408/33.

XX P-PSDB; ABB97310.

PT An isolated polynucleotide for treating diseases associated with its
 encoded polypeptide such as cancer and multiple sclerosis.

XX Claim 1; SEQ ID NO 134; 509pp; English.

XX The present invention provides the protein and coding sequences of 444
 CC novel human proteins. These were isolated from expressed sequences tags
 CC (ESTs). They can be used to stimulate cell growth, to regulate
 CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
 CC e.g. in burn treatment, to regulate the immune system e.g. to treat
 CC multiple sclerosis, to regulate haemostasis or thrombolysis e.g. to treat
 CC infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke
 CC and cancer, to screen for drugs, to treat inflammatory conditions e.g.
 CC rheumatoid arthritis, and to treat nervous system disorders e.g.
 CC Parkinson's disease. The present sequence is a coding sequence of the

CC invention
XX
SQ Sequence 3267 BP; 628 A; 1101 C; 927 G; 611 T; 0 U; 0 Other;

Alignment Scores:	1.23e-124	Length:	3267
Pred. No.:	Score:	Matches:	264
	148.00	Conservative:	0
Percent Similarity:	98.51%	Mismatches:	2
Best Local Similarity:	98.51%	Indels:	4
Query Match:	48.84%	Gaps:	0
DB:	6		

US-10-047-021-86 (1-303) x ABN59723 (1-3267)

1	MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeu	20
35	ATGGGCTCTGGAGGACAGACAGCTCTCTGGGGGGCAGGGTTCCCTGGCTCTGGCTGCTCGT	94
21	LeuIleMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp	40
95	CTCATCATGGGAGGCGATGGCTCAGACTCTCCCGGCCCCAGATCTTAGTCCACCCCGAGAC	154
41	GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProPr	60
155	CAGCTGTTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCAC	213
60	ProThrIleArgTrpIleLeuAenGlyGlnProLeuSerMetValProAspProHis	80
214	TCCACCAATCGCTGTGTGCTGAATGGCAGCCCTCAGCATGGTGCCTCCCGGGGACATGCCA	273
80	SHisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHi	100
274	CCACCTCCTGCATGGAGCCCTTCTGCTGCTACAGCCCCCTTCCCGGGGACATGCCA	333
100	AspGlyGlnIleLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgIle	120
334	CGATGGCCAGGCGCTGTCCACAGACCTCTGGGTGTCTACACATGTGAGCGCAGCAACCGGCT	393
120	uGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheG	140
394	TGGCAGCGGAGTACAGAGGCGCTCGGCTGTCTGTGGCTGTCTCCGGAGGATTTCCA	453
140	nileGlnProArgAspMetValAlaValValGlyGlnPheThrLeuGluCysGlyPr	160
454	GATCCAGCTCTGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGC	513
160	oProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyIlyPProLeuAlaIle	180
514	GCCTTGGGGGCCACCCAGAGCCCAACAGCTCTCATGTGTGAAAGATGGAAACCCCTGGCCCT	573
180	uGlnProGlyIArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSe	200
574	CCAGCCCCGAGAGGCACACAGTGTCCGGGGGTCCCTGCTGATGGCAAGAGCAGAGAGAG	633
200	rAspGlu***-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgA	220
634	TGACGAAGG-GACCTACATGTGTGTGGCCACCAACAGCGCAGGACATATGGGAGAGCGCG	692
220	IaAlaArgValSerIleGlnIleGlnIleProGlnAspTyrThrGluProValGluLeuLeuAlaV	240
693	CAGCCCCGGTTTCCATCCAGAGAGCCACAGACATACAGGAGCTGTGGAGCTTCTGGCTG	752
240	AlaTrqIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysP	260
753	TCCGNATTCACTGGAAAATGTGCATCTGTGAACCGGATCTTCGACAGGGCCCCCAGC	812
260	roArgProAlaValTrpIleu	266
813	CTAGACCGCGGTGTGGCTC	832

RESULT 4
ABK87137
ID ABK87137

XX	ABK87137;	
AC	XX	
XX	07-OCT-2002 (first entry)	
DT	XX	
XX	CDNA human ECSM4 protein.	
DE	XX	
XX	Human; endothelial cell-specific molecule 4; ECSM4; neovasculature;	
XX	imaging vascular endothelium; proliferative disease; cancer; psoriasis;	
XX	diabetic retinopathy; atherosclerosis; menorrhagia; endothelial damage;	
XX	tumour neovasculature; cardiac disease; endometriosis; hypoxic condition;	
XX	angiogenesis; cytostatic; cardiant; gene; ss.	
XX	Homo sapiens.	
OS	XX	
XX	Key Location/Qualifiers	
XX	FT CDS 70..3384	
XX	FT FT /*tag= a	
XX	FT FT /product= "ECSM4"	
XX	WO200236771-A2.	
XX	10-MAY-2002.	
XX	06-NOV-2001; 2001WO-GB004906.	
XX	06-NOV-2000; 2000US-0245566P.	
XX	07-MAR-2001; 2001US-0273662P.	
XX	(IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.	
XX	Bicknell R, Huminiecki L;	
XX	WPI: 2002-508120/54.	
XX	P-PSDB; AAU99419.	
XX	Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for	
XX	imaging, diagnosing and treating a condition involving vascular	
XX	endothelium e.g. cancer, cardiac disease, endometriosis, diabetes.	
XX	Disclosure; Fig 12; 248pp; English.	
XX	The present invention relates to endothelial cell-specific molecule 4	
XX	(ECSM4), and the polynucleotide sequences encoding it. The ECSM4 proteins	
XX	are useful for imaging vascular endothelium in the body of an individual,	
XX	and for diagnosing and treating a proliferative disease or condition	
XX	involving the vascular endothelium (preferably, neovasculature) such as	
XX	cancer, psoriasis, diabetic retinopathy, atherosclerosis or menorrhagia.	
XX	The ECSM4 proteins are also useful in the manufacture of diagnostic or	
XX	prognostic agent for such conditions. The proteins are also useful for	
XX	detecting endothelial damage or activation, detecting a tumour or tumour	
XX	neovasculature, cardiac disease, or endometriosis by detecting the amount	
XX	of ECSM4 present in a sample. The polynucleotide sequences encoding ECSM4	
XX	are useful in gene therapy for treating a hypoxic condition such as	
XX	cancer, cardiac disease, endometriosis or atherosclerosis and in the	
XX	manufacture of medicaments for treating the above disease. The sequences	
XX	are useful for modulating angiogenesis in an individual. The present	
XX	sequence encodes human ECSM4 protein	
XX	Sequence 3715 BP; 725 A; 1239 C; 1053 G; 698 T; 0 U; 0 Other;	
XX	Alignment Scores:	
XX	Pred. No.: 1..398-124 Length: 3715	
XX	Score: 148.00 Matches: 264	
XX	Percent Similarity: 98.51% Conservative: 0	
XX	Best Local Similarity: 98.51% Mismatches: 2	
XX	Query Match: 48.94% Indels: 4	
XX	DB: 6 Gaps: 0	
XX	US-10-047-021-86 (1-303) x ABK87137 (1-3715)	
XX	1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20	

Db	70	ATGGGCTCGAGGAGACACGCTCTCGGGGGGAGGGTTCCCTCTGCTGCTCCTG	129	XX	08-MAR-1999;	99WO-US005028.
Qy	21	LeuileMetGlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAsp	40	XX	10-MAR-1998;	98US-0077450P.
Db	130	CTCATGTGGAGGATGGCTCAGGACTCCCGCCCGACATCTAGTCCACCCCGAGGAC	189	PR	11-MAR-1998;	98US-0077641P.
Qy	41	GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPr	60	PR	11-MAR-1998;	98US-0077649P.
Db	190	CAGCTGTTCCAGGGCCCTGGCCCTGCAGATGAGCTGCCAAGCTCAGGCCAGCCACC	248	PR	12-MAR-1998;	98US-0077791P.
Qy	60	oProThrIleArgTTrpLeuLeuAsnGlyGlnProLeuSerMetValProAspProHi	80	PR	13-MAR-1998;	98US-0078004P.
Db	249	TCCACCATCCGCTGGTGTGTAATGGGAGCCCTGAGCATGTGTCCTCCCGCCAGACCCACA	308	PR	17-MAR-1998;	98US-00040220.
Qy	80	sHisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHi	100	PR	20-MAR-1998;	98US-0078866P.
Db	309	CCACCTCTCTGCTGATGGGACCTTTCTGTCTACAGCCCTGCTCCCGGGGACATGCCCA	368	PR	20-MAR-1998;	98US-0078910P.
Qy	100	sAspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgIe	120	PR	20-MAR-1998;	98US-0078936P.
Db	369	CGATGGCCAGCCCTGTCCACAGACCTGGGTGTCTACATGTGAGCCAGCAACCCGGCT	428	PR	20-MAR-1998;	98US-0078939P.
Qy	120	uGlyThrAlaValSerArgGlyAlaArgIleuSerValAlaValLeuArgGluAspPheG	140	PR	25-MAR-1998;	98US-0079294P.
Db	429	TGGCAGGGCAGTCAGCAGAGCGCTGGCTGTCTGTGGCTGTCTCCCGGAGGATTTCCA	488	PR	26-MAR-1998;	98US-0079656P.
Qy	140	nIleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPr	160	PR	27-MAR-1998;	98US-0079664P.
Db	489	GATCCAGCCCTCGGACATGTGTGCTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT	548	PR	27-MAR-1998;	98US-0079689P.
Qy	160	oProTTrpGlyHisProGluProThrValSerTTrpTTrpLysAspGlyLysProLeuAlaIe	180	PR	27-MAR-1998;	98US-0079728P.
Db	549	GCCTCGGGCCAGCCAGAGCCACAGTCTCATGTGGTGGTGGTGGTGGTGGTGGTGGT	608	PR	27-MAR-1998;	98US-0079786P.
Qy	180	uGlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSe	200	PR	30-MAR-1998;	98US-0079920P.
Db	609	CCAGCCCGAAGGACACACATGTCTCGGGGGTCTCTGCTGTATGTCAGAGCAGAGAGAG	668	PR	31-MAR-1998;	98US-0080105P.
Qy	200	rAspGlu***-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgA	220	PR	31-MAR-1998;	98US-0080107P.
Db	669	TGACGAAAGG-GACCTACATGTGTGGCCACCAACAGCGCAGGACATAGGAGAGCGCG	727	PR	31-MAR-1998;	98US-0080165P.
Qy	220	laalaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlav	240	PR	01-APR-1998;	98US-0080333P.
Db	728	CAGCCCGGGTTTCATCCAGAGCCCGCAGGACTACAGGAGCCTGTGGAGCTTCTGGCTG	787	PR	08-APR-1998;	98US-0080334P.
Qy	240	alArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysP	260	PR	08-APR-1998;	98US-0081049P.
Db	788	TGCGAATCAGCTGGAAAATGTGACACTGTCTGAACCCGATCTGTCAGAGGGCCCCAAGC	847	PR	08-APR-1998;	98US-0081070P.
Qy	260	roArgProAlaValTTrpLeu 266		PR	09-APR-1998;	98US-0081195P.
Db	848	CTAGACCGGGGTGTGGCTC 867		PR	09-APR-1998;	98US-0081203P.
RESULT 5						98US-0081229P.
ID	AAZ34069 standard; cDNA; 3716 BP.					98US-0081817P.
XX	AC AAZ34069;					98US-0081838P.
XX	AC AAZ34069;					98US-0081952P.
DT	07-DEC-1999 (first entry)					98US-0082568P.
DE	Human PRO860 nucleotide sequence.					98US-0082700P.
KW	Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;					98US-0082804P.
KW	probe; blood coagulation disorder; cancer; cellular adhesion disorder;					98US-0082767P.
KW	secreted protein; transmembrane protein; ss.					98US-0082796P.
OS	Homo sapiens.					98US-0083336P.
XX	WO9946281-A2.					98US-0083322P.
XX	16-SEP-1999.					98US-0083392P.
PD						98US-0083495P.

PR 30-DEC-1999; 99WO-US031274.
PR 03-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart JA, Tumas D, Williams PM, Wood WI;
XX WPI; 2000-611443/58.
DR P-PSDB; AAB44272.
XX
XX Novel PRO polypeptides and polynucleotides used in detection methods, to
PT target bioactive molecules to specific cells, and to modulate cellular
PT activities.
XX
XX Claim 2; Fig 76; 636pp; English.
XX
XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
CC tag) sequences which encode secreted or transmembrane PRO polypeptides.
CC The PRO polynucleotides and polypeptides have cytosolic activity. The
CC polynucleotides and polypeptides can be used for detecting the presence
CC of PRO polypeptides in samples, for linking bioactive molecules to cells
CC and for modulating biological activities of cells, using the polypeptides
CC for specific targeting. The polypeptide targeting can be used to kill the
CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
CC provide specific targeting of bioactive molecules to cells. AAC78600 to
CC AAC78987 represent PCR primers and probes used in the isolation of the
CC PRO polynucleotide sequences
XX
XX Sequence 3716 BP; 757 A; 1225 C; 1032 G; 702 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 1.39e-124 Length: 3716
Score: 148.00 Matches: 261
Percent Similarity: 98.49% Conservative: 0
Best Local Similarity: 98.49% Mismatches: 2
Query Match: 48.84% Indels: 4
DB: 3 Gaps: 0

US-10-047-021-86 (1-303) x AAC78502 (1-3716)

Qy 4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuMet 23
Db 1 GGAGGAGACAGCTTCTGGGGGGGAGGGTTCCTGCTGCTGCTGCTCATCATG 60
Qy 24 GlyGlyMetAlaGlnAspSerProGlnInLeuValHisProGlnAspGlnLeuPhe 43
Db 61 GGAGGATGGCTCAGGACTCCCGCCCGCCAGATCCTAGTCCACCCCGCCAGGACCTGTC 120
Qy 44 GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProThrIle 63
Db 121 CAGGGCCCTGGCCCTGCCAGGATGAGTGCCA-AGCTCAGGCGGAGCAGCTCCACCAT 179
Qy 63 eArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisLeuLe 83
Db 180 CCGCTGGTTGCTGAATGGGAGCCCTTGGATGCTGCTGCTGCTGCTGCTGCTGCT 239
Qy 83 uProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyG 103
Db 240 GCCTGATGGGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 299
Qy 103 nAlaLeuSerThrAspLeuGlyValTyThrCysGluAlaSerAsnArgLeuGlyThrAl 123
Db 300 GGCCCTGTCCACAGACCTGGGTGTCTACATGTGAGGCGGAGCAGCCGCTGGCAGGC 359
Qy 123 aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGlnAspPheGlnIleGlnPr 143
Db 360 AGTCAGCAGAGCGGCTCGGCTGTCTGTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCT 419

Qy 143 oArgAspMetValAlaValValGlyGlnGlnPheThrLeuGlyCysGlyProProTrpG 163
Db 420 TCGGACATGGTGGCTGTGGTGGGAGACAGTTTACTCTGGAATGTGGCGCCCTGGGG 479
Qy 163 yHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProG 183
Db 480 CCACCCAGAGCCACAGTCTCATGTGGAAGATGGGAAACCCCTGGGCTCCAGCCCGG 539
Qy 183 yArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGlyLysSerAspGlu 203
Db 540 AAGGCACACAGTGTCCGGGGGTCCCTGCTGATGCAAGAGCAGAGAGAGTGCAGAGG 599
Qy 203 *-ThrTyMetCysValAlaThrAenSerAlaGlyHisArgGlySerArgAlaArgV 223
Db 600 -GACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGAGAGCGCGCAGCCCGG 658
Qy 223 alserIleGlnGlnProGlnAspTyThrGluProValGluLeuLeuAlaValArgIleG 243
Db 659 TTTCCATCCAGGAGCCCGGAGGACTACACGAGGCTTGTGGAGCTTCTGCTGTGCGAATTC 718
Qy 243 InLeuGluAsnValThrLeuLeuAenProAspProAlaGluGlyProLysProArgProA 263
Db 719 AGCTGGAAATGTGACACTGCTGAACCCGGATCTCTGCAGAGGGCCCGCAGCTAGACCGG 778
Qy 263 laValTrpLeu 266
Db 779 CGGTGTGGCTC 789
RESULT 7
ACD42602
ID ACD42602 standard; cDNA; 3716 BP.
XX
XX ACD42602;
XX
XX 09-SEP-2003 (first entry)
XX
XX Novel human secreted and transmembrane protein PRO860 cDNA.
XX
XX Human; secreted and transmembrane protein; PRO; virucide; gene therapy;
KW cell death; growth induction cascade; blood coagulation cascade;
KW viral infection; gene; ss.
XX
XX Homo sapiens.
XX
XX US2003050239-A1.
XX
XX 13-MAR-2003.
XX
XX 15-OCT-2001; 2001US-00978191.
XX
XX 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-0080420P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.

PR 30-MAR-1998;	98US-0079920P.	PR 30-JUL-1998;	98US-0094651P.
PR 30-MAR-1998;	98US-0079923P.	PR 11-SEP-1998;	98US-0100038P.
PR 31-MAR-1998;	98US-0080105P.	PR 07-OCT-1998;	98US-00168978.
PR 31-MAR-1998;	98US-0080107P.	PR 07-OCT-1998;	98WO-US02114.
PR 31-MAR-1998;	98US-0080165P.	PR 06-NOV-1998;	98US-00184216.
PR 31-MAR-1998;	98US-0080194P.	PR 20-NOV-1998;	98US-00187368.
PR 01-APR-1998;	98US-0080327P.	PR 20-NOV-1998;	98US-0109304P.
PR 01-APR-1998;	98US-0080328P.	PR 07-DEC-1998;	98WO-US024855.
PR 01-APR-1998;	98US-0080333P.	PR 22-DEC-1998;	98US-00202054.
PR 08-APR-1998;	98US-0080334P.	PR 22-DEC-1998;	98US-00218517.
PR 08-APR-1998;	98US-0081049P.	PR 23-DEC-1998;	98US-0113296P.
PR 08-APR-1998;	98US-0081070P.	PR 05-JAN-1999;	98US-0113621P.
PR 09-APR-1998;	98US-0081071P.	PR 05-JAN-1999;	98WO-US000106.
PR 09-APR-1998;	98US-0081195P.	PR 08-MAR-1999;	98US-00254465.
PR 09-APR-1998;	98US-0081203P.	PR 10-MAR-1999;	98WO-US005028.
PR 15-APR-1998;	98US-0081229P.	PR 10-MAR-1999;	98US-00265686.
PR 15-APR-1998;	98US-0081817P.	PR 12-MAR-1999;	98WO-US005190.
PR 15-APR-1998;	98US-0081819P.	PR 12-MAR-1999;	98US-00287213.
PR 15-APR-1998;	98US-0081838P.	PR 29-MAR-1999;	98US-0123957P.
PR 15-APR-1998;	98US-0081952P.	PR 12-APR-1999;	98US-0126773P.
PR 15-APR-1998;	98US-0081955P.	PR 21-APR-1999;	98US-00284291.
PR 21-APR-1998;	98US-0082568P.	PR 26-APR-1999;	98US-0130232P.
PR 21-APR-1998;	98US-0082569P.	PR 28-APR-1999;	98US-0131022P.
PR 22-APR-1998;	98US-0082700P.	PR 14-MAY-1999;	98US-0131445P.
PR 22-APR-1998;	98US-0082704P.	PR 14-MAY-1999;	98US-00311832.
PR 22-APR-1998;	98US-0082797P.	PR 14-MAY-1999;	98US-0134287P.
PR 22-APR-1998;	98US-0082804P.	PR 02-JUN-1999;	98WO-US010733.
PR 23-APR-1998;	98US-0082796P.	PR 16-JUN-1999;	98WO-US012252.
PR 27-APR-1998;	98US-0083336P.	PR 23-JUN-1999;	98US-0139557P.
PR 28-APR-1998;	98US-0083322P.	PR 07-JUL-1999;	98US-0141037P.
PR 29-APR-1998;	98US-0083392P.	PR 26-JUL-1999;	98US-0142680P.
PR 29-APR-1998;	98US-0083495P.	PR 28-JUL-1999;	98US-0145698P.
PR 29-APR-1998;	98US-0083496P.	PR 25-AUG-1999;	98US-0146222P.
PR 29-APR-1998;	98US-0083500P.	PR 25-AUG-1999;	98US-00380137.
PR 29-APR-1998;	98US-0083505P.	PR 25-AUG-1999;	98US-00380138.
PR 29-APR-1998;	98US-0083554P.	PR 29-OCT-1999;	98US-00380142.
PR 29-APR-1998;	98US-0083558P.	PR 30-NOV-1999;	98US-0162506P.
PR 30-APR-1998;	98US-0083559P.	PR 02-DEC-1999;	98WO-US028313.
PR 30-APR-1998;	98US-0083742P.	PR 02-DEC-1999;	98WO-US028551.
PR 05-MAY-1998;	98US-0084366P.	PR 16-DEC-1999;	98WO-US028565.
PR 06-MAY-1998;	98US-0084414P.	PR 30-DEC-1999;	98WO-US030095.
PR 06-MAY-1998;	98US-0084414P.	PR 30-DEC-1999;	98WO-US031243.
PR 07-MAY-1998;	98US-0084498P.	PR 05-JAN-2000;	98WO-US031274.
PR 07-MAY-1998;	98US-0084600P.	PR 06-JAN-2000;	2000WO-US000219.
PR 07-MAY-1998;	98US-0084627P.	PR 11-FEB-2000;	2000WO-US000277.
PR 07-MAY-1998;	98US-0084637P.	PR 18-FEB-2000;	2000WO-US003565.
PR 07-MAY-1998;	98US-0084639P.	PR 24-FEB-2000;	2000WO-US004341.
PR 07-MAY-1998;	98US-0084640P.	PR 02-MAR-2000;	2000WO-US005004.
PR 13-MAY-1998;	98US-0085323P.	PR 10-MAR-2000;	2000WO-US005841.
PR 13-MAY-1998;	98US-0085338P.	PR 21-MAR-2000;	2000WO-US006319.
PR 13-MAY-1998;	98US-0085339P.	PR 30-MAR-2000;	2000WO-US007532.
PR 15-MAY-1998;	98US-0085573P.	PR 17-MAY-2000;	2000WO-US008439.
PR 15-MAY-1998;	98US-0085579P.	PR 22-MAY-2000;	2000WO-US013705.
PR 15-MAY-1998;	98US-0085580P.	PR 30-MAY-2000;	2000WO-US014042.
PR 15-MAY-1998;	98US-0085582P.	PR 02-JUN-2000;	2000WO-US014941.
PR 15-MAY-1998;	98US-0085689P.	PR 28-JUL-2000;	2000WO-US015264.
PR 15-MAY-1998;	98US-0085697P.	PR 24-AUG-2000;	2000WO-US020710.
PR 15-MAY-1998;	98US-0085700P.	PR 08-NOV-2000;	2000WO-US023328.
PR 15-MAY-1998;	98US-0085704P.	PR 27-NOV-2000;	2000US-00709238.
PR 18-MAY-1998;	98US-0086023P.	PR 01-DEC-2000;	2000US-00723749.
PR 22-MAY-1998;	98US-0086392P.	PR 20-DEC-2000;	2000WO-US032678.
PR 22-MAY-1998;	98US-0086414P.	PR 20-DEC-2000;	2000US-00747259.
PR 22-MAY-1998;	98US-0086430P.	PR 28-FEB-2001;	2000WO-US034956.
PR 22-MAY-1998;	98US-0086486P.	PR 22-MAR-2001;	2001WO-US006520.
PR 28-MAY-1998;	98US-0087098P.	PR 22-MAR-2001;	2001US-00816744.
PR 28-MAY-1998;	98US-0087106P.	PR 10-MAY-2001;	2001US-00816920.
PR 28-MAY-1998;	98US-0087208P.	PR 10-MAY-2001;	2001WO-US009552.
PR 26-JUN-1998;	98US-00105413.	PR 25-MAY-2001;	2001US-00854208.
PR 26-JUN-1998;	98US-0030863P.	PR 01-JUN-2001;	2001WO-US017092.
PR 01-JUL-1998;	98US-0091010P.	PR 01-JUN-2001;	2001US-00872035.
PR 01-JUL-1998;	98US-0091359P.	PR 01-JUN-2001;	2001WO-US017800.

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PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001US-00886342.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021066.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;

Alignment Scores:
Pred. No.: 1.39e-124 Length: 3716
Score: 148.00 Matches: 261
Percent Similarity: 98.49% Conservative: 0
Best Local Similarity: 98.49% Mismatches: 2
Query Match: 48.84% Indels: 4
DB: 7 Gaps: 0

US-10-047-021-86 (1-303) x ACD42602 (1-3716)

Qy 4 GlyGlyAspSerLeuLeuGlyArgGlySerLeuProLeuLeuLeuLeuMet 23
Db 1 GGAGGACAGACCTCCCTGGGGGAGGGGTTCCCTGCTGCTGCTGCTCATCATG 60
Qy 24 GlyGlyMetAlaGlnAspSerProGlnIleuValHisProGlnAspGlnLeuPhe 43
Db 61 GGAGGACAGGCTCAGGACTCCCGCCCGAGATCTAGTCCACCCCGAGGACGAGTGTTC 120
Qy 44 GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProThrIle 63
Db 121 CAGGCGCTGGCTGCGAGGATGAGTGCCA-AGCCTCAGGCGGACACCTCCACCAT 179
Qy 63 eArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProAspProHisIleuLeu 83
Db 180 CCGCTGCTGCTGAATGGGAGCCCTGAGCATGGTCCCGCCAGACCCACACCATCTCT 239
Qy 83 uProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyG 103
Db 240 GCCTGATGGAGACCTTCTGTGCTACAGCCCTGCGCGGGACATGCCACCATGGCCA 299
Qy 103 nAlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAl 123
Db 300 GGCCCTGTCACAGACCTGGGTGTCTACATGTGAGGCGAGCAACCGGCTTGCGACGC 359
Qy 123 aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPr 143
Db 360 AGTCAGCAGAGGCGCTCGGCTGTCTGTGGTGTCTCCCGGAGAGATTCAGATCCAGCC 419
Qy 143 oArgAspMetValAlaValGlyGluGlnPheThrLeuGluCysGlyProProTrpG 163
Db 420 TCGGACATGCTGGCTGTGGTGGTGGAGCAGTTTACTCTGGAATGTGGCGCGCTGGGG 479
Qy 163 yHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProG 183
Db 480 CCACCCAGAGCCACAGTCTCATGTGGAGAGTGGGAAACCCCTGCGCCCTCCAGGCCGG 539
Qy 183 yArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu** 203
Db 540 AAGGACACACAGTGTCCGGGGGTCCCTGCTGATGGCAAGGACAGAGAGTGCAGAGG 599
Qy 203 *-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgV 223
Db 600 -GACCTACATGTGTGGCCACCAACAGCGCAGGACATAGGAGAGCGCGGCGAGCCCGGG 658
Qy 223 alSerIleGlnGluProGlnAspTrpThrGluProValGluLeuLeuAlaValArgIleG 243
Db 659 TTTCCATCCAGAGCCCGGAGACTACAGGAGCTGTGGAGCTTCTGGCTGTGGAAATTC 718
Qy 243 lnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProA 263

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Db 719 AGCTGGAATAATGTGACACTGTGAACCGGATCTGCAGAGGGGCCCAAGCCTAGACCGG 778
Qy 263 laValTrpLeu 266
Db 779 CGGTGTGGCTC 789
RESULT 8
ACA63637
ID ACA63637 standard; cDNA; 3716 BP.
XX
AC ACA63637;
XX
DT 16-JUN-2003 (first entry)
XX
DE Novol human secreted and transmembrane protein PRO860 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW antiarteriosclerotic; cardian; anti-infertility; anti-HIV; cytostatic;
KW antidiabetic; gene therapy; inflammatory disease; organ failure;
KW atherosclerosis; cardiac injury; infertility; birth defect;
KW premature aging; AIDS; cancer; diabetic complication; chromosome mapping;
KW gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor;
KW tissue typing; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002192706-A1.
PD 19-DEC-2002.
XX
PF 24-OCT-2001; 2001US-00999832.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 13-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0065364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-0040220.
PR 20-MAR-1998; 98US-0078888P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080103P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080163P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080328P.
PR 01-APR-1998; 98US-0080333P.
PR 01-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 09-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081222P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081819P.
PR 15-APR-1998; 98US-0081838P.

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Db 779 CGGTGTGGCTC 789
RESULT 9
ACAV1801
ID ACA71801 standard; cDNA; 3716 BP.
XX
AC ACA71801;
XX
XX
DT 11-AUG-2003 (first entry)
XX
XX Human secreted and transmembrane polypeptide PRO860 cDNA.
DE XX
XX Human; ss; gene; thrombolytic agent; interferon; interleukin; cytokine;
KW erythropoietin; colony stimulating factor; cancer; colorectal carcinoma;
KW apoptosis related condition; AIDS; amyotrophic lateral sclerosis;
KW inflammatory disease; asthma; atherosclerosis; neurodegenerative disease;
KW gastrointestinal disorder; Alzheimer's disease; Parkinson's disease;
KW hypertension; myocardial ischaemia; kidney disease; carcinogenesis;
KW glomerulonephritis; lung disease; pulmonary hypertension; pre-eclampsia;
KW bronchial asthma; gastric ulcer; renal failure; cardiovascular disease;
KW inflammatory bowel disease; reproductive disorder; premature labour.
XX
OS Homo sapiens.
XX
XX US2002177553-A1.
XX
XX 28-NOV-2002.
XX
XX 15-OCT-2001; 2001US-00978192.
XX
PR 17-OCT-1997; 97US-00622250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040320.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 26-JUN-1998; 98US-00105413.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98US-0021141.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98US-00204855.
PR 07-DEC-1998; 98US-00202054.
PR 22-DEC-1998; 98US-00218517.
PR 05-JAN-1999; 98US-0000106.
PR 05-MAR-1999; 98US-00254465.
PR 08-MAR-1999; 98US-00005028.
PR 10-MAR-1999; 98US-00265566.
PR 10-MAR-1999; 98US-00005190.
PR 12-MAR-1999; 98US-00267213.
PR 12-APR-1999; 98US-00284291.
PR 14-MAY-1999; 98US-00311832.
PR 14-MAY-1999; 98US-00310733.
PR 02-JUN-1999; 98US-00012352.
PR 25-AUG-1999; 98US-00380137.

PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 20-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00916585.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Pong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin LJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PW, Wood WI;
XX WPI; 2003-328499/31.
DR P-PSDB; ABU84904.
DR
XX
XX New isolated PRO polypeptides e.g. PRO213, PRO274 and PRO300, for use as
PT pharmaceuticals, diagnostics, biosensors and bioreactors, for identifying
PT modulators of receptor-ligand interactions.
XX
XX Claim 2; SEQ ID NO 210; 55pp; English.
XX
XX The invention relates to an isolated secreted and transmembrane
CC polypeptide, designated as PRO polypeptide. The PRO polypeptide is useful
CC in PRO polypeptide detection methods. The PRO polypeptide is useful for
CC linking a bioactive molecule to a cell. The PRO polypeptide or an
CC antibody against it is useful for modulating a biological activity of a
CC cell. The PRO polypeptide is useful in industrial applications including
CC pharmaceuticals, diagnostics, biosensors and bioreactors. The PRO
CC polypeptide is also useful as a thrombolytic agent, interferon,
CC interleukin, erythropoietin, colony stimulating factor and other
CC cytokines. The PRO polypeptide is useful for treating disease such as

CC cancer e.g. colorectal carcinoma; apoptosis related conditions e.g. AIDS,
CC amyotrophic lateral sclerosis; inflammatory disease e.g. asthma,
CC atherosclerosis; neurodegenerative disease e.g. Alzheimer's disease,
CC Parkinson's disease; cardiovascular disease e.g. hypertension and
CC myocardial ischaemia; kidney disease e.g. renal failure and
CC glomerulonephritis; lung disease e.g. pulmonary hypertension, bronchial
CC asthma; gastrointestinal disorders e.g. gastric ulcer and inflammatory
CC bowel disease; reproductive disorders e.g. premature labour and
CC preclampsia; carcinogenesis. The present sequence represents a cDNA
CC encoding a PRO polypeptide of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20020177553
XX

SQ Sequence 3716 BP; 757 A; 1225 C; 1032 G; 702 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,398-124	Length:	3716
Score:	148.00	Matches:	261
Percent Similarity:	98.49%	Conservative:	0
Best Local Similarity:	98.49%	Mismatches:	2
Query Match:	48.84%	Indels:	4
DB:	7	Gaps:	0

US-10-047-021-86 (1-303) x ACA71801 (1-3716)

QY	4	GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuMet	23
DB	1	GGAGGAGACAGCTCTGGGGGGGAGGGTTCCCTGCTGCTGCTCTGCTCATCATG	60
QY	24	GlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPhe	43
DB	61	GGAGCATGGCTCAGGACTCCCGCCCGCAGATCTCTAGTCCACCCGAGCACAGCTGTT	120
QY	44	GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProThrIle	63
DB	121	CAGGGCCCTGGCCCTGCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACCTCCACCAT	179
QY	63	eArgTrpLeuLeuGlnGlnProLeuSerMetValProAspProHisIleLeuLe	83
DB	180	CCGCTGGTGTGATGGGAGCCCTGAGCATGGTCCCGCCAGCACACACACCTCT	239
QY	83	uProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyG	103
DB	240	GCCTGATGGGACCTTCTGCTGCTACAGCCCTGCCCGGGGACATGCCACCATGGCCA	299
QY	103	nAlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAl	123
DB	300	GGCCCTGTCCACAGACCTGGGTGTCTACATGTGAGCCAGCAACCGGCTTGCCACGG	359
QY	123	avalSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPr	143
DB	360	AGTCAGCAGAGCCCTCGCTGCTGTGGCTGTCTCCGGGAGATTCAGATCCAGCC	419
QY	143	oArgAspMetValAlaValGlyGlnPheThrLeuGluCysGlyProProTrpG	163
DB	420	TCGGGACATGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCGCCCTGGGG	479
QY	163	yHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProG	193
DB	480	CCACCCAGAGCCCATGCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCGG	539
QY	183	yArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu**	203
DB	540	AAGGCACACAGTGTCCGGGGGTCCTGCTGATGGCAAGACAGAGAGAGTGCAGAGG	599
QY	203	*-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgV	223
DB	600	-GACCTACATGTGTGGCCACCAACAGCGAGCATAGGGAGAGCCGCGAGCCCGGG	658
QY	223	alSerIleGlnProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleG	243
DB	659	TTTCCATCCAGAGCCCAAGACTACAGGAGGCTGTGGAGCTTCTGGCTGTCCGATTC	718

QY	243	InLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgP:OA	263
DB	719	AGCTGGAAATGTGACACTGCTGACCCGGATCTTGCAGAGGGCCCCCAGGCTAGACCGG	778
QY	263	laValTrpLeu 266	
DB	779	CGGTGGGCTC 789	
RESULT 10			
ABX92441			
ID	ABX92441	standard; cDNA; 3716 BP.	
XX	AC	ABX92441;	
XX	XX	08-MAY-2003 (first entry)	
XX	XX	cDNA encoding human PRO860 polypeptide.	
DE	XX	Human; PRO polypeptide; secreted and transmembrane protein;	
XX	KW	immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;	
KW	KW	cardiac insufficiency; nervous system disorder; kidney disorder;	
KW	KW	bone disorder; cartilage disorder; arthritis; tumour; wound healing;	
KW	KW	genetic disorder; cytostatic; antidiabetic; antiinflammatory;	
KW	KW	antiarthritic; anti-tumour; vulnerary; antianaemic; dermatological;	
KW	KW	cardiant; gene; ss.	
XX	XX	Homo sapiens.	
OS	XX	US2002169284-Al.	
PN	XX	14-NOV-2002.	
PD	XX	16-OCT-2001; 2001US-00978697.	
XX	XX	26-MAY-1981; 81US-00267213.	
PR	PR	17-OCT-1997; 97US-0062250P.	
PR	PR	03-NOV-1997; 97US-0064249P.	
PR	PR	13-NOV-1997; 97US-0065311P.	
PR	PR	21-NOV-1997; 97US-0066364P.	
PR	PR	10-MAR-1998; 98US-0077450P.	
PR	PR	11-MAR-1998; 98US-0077632P.	
PR	PR	11-MAR-1998; 98US-0077641P.	
PR	PR	11-MAR-1998; 98US-0077649P.	
PR	PR	12-MAR-1998; 98US-0077791P.	
PR	PR	13-MAR-1998; 98US-0078004P.	
PR	PR	17-MAR-1998; 98US-00040220.	
PR	PR	20-MAR-1998; 98US-0078886P.	
PR	PR	20-MAR-1998; 98US-0078910P.	
PR	PR	20-MAR-1998; 98US-0078936P.	
PR	PR	20-MAR-1998; 98US-0078939P.	
PR	PR	25-MAR-1998; 98US-0079294P.	
PR	PR	26-MAR-1998; 98US-0079656P.	
PR	PR	27-MAR-1998; 98US-0079663P.	
PR	PR	27-MAR-1998; 98US-0079664P.	
PR	PR	27-MAR-1998; 98US-0079689P.	
PR	PR	27-MAR-1998; 98US-0079728P.	
PR	PR	27-MAR-1998; 98US-0079786P.	
PR	PR	30-MAR-1998; 98US-0079920P.	
PR	PR	30-MAR-1998; 98US-0079923P.	
PR	PR	26-JUN-1998; 98US-00105413.	
PR	PR	07-OCT-1998; 98US-00168978.	
PR	PR	02-NOV-1998; 98WO-US021141.	
PR	PR	06-NOV-1998; 98US-00187368.	
PR	PR	20-NOV-1998; 98WO-US024855.	
PR	PR	07-DEC-1998; 98US-00202054.	
PR	PR	22-DEC-1998; 98US-00218517.	
PR	PR	05-JAN-1999; 99WO-US000106.	
PR	PR	08-MAR-1999; 99US-00254465.	
PR	PR	10-MAR-1999; 99WO-US005028.	
PR	PR	10-MAR-1999; 99US-00265686.	
PR	PR	10-MAR-1999; 99WO-US005190.	

sequence with at least 80% identity to: (a) a nucleotide encoding any of 94 PRO polypeptides whose sequences are fully defined in the specification; or (b) any of 94 nucleotide sequences fully defined in the specification; or the full length coding sequence of any these 94 nucleotide sequences. Also included are an isolated PRO polypeptide scoring at least 80% positives when compared to any of the PRO polypeptide sequences cited above (or an isolated PRO polypeptide having at least 80% amino acid sequence identity to: (a) an amino acid sequence encoded by the nucleotide deposited with ATCC numbers listed in the specification; (b) the PRO polypeptide, lacking its associated signal peptide; or (c) an extracellular domain of the PRO polypeptide, with or lacking its associated signal peptide), a vector comprising the nucleic acid molecule, a host cell comprising the vector (and producing a PRO polypeptide), a chimeric molecule comprising the PRO polypeptide fused to a heterologous amino acid sequence and an anti-PRO antibody. The PRO polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer, colorectal cancer, sarcoma, leukaemia or lymphoma), inflammatory disease, necrosis, atherosclerosis, infertility, premature aging, psoriasis, rheumatoid arthritis, renal disease, arthritis, immune-mediated alopecia, stroke, encephalitis, hepatitis, or multiple sclerosis in mammals. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases, and in the diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The present sequence encodes a PRO polypeptide

XX SQ Sequence 3716 BP; 757 A; 1225 C; 1032 G; 702 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.39e-124	Length:	3716
Score:	148.00	Matches:	261
Percent Similarity:	98.49%	Conservative:	0
Best Local Similarity:	98.49%	Mismatches:	2
Query Match:	48.84%	Indels:	4
DB:	7	Gaps:	0

US-10-047-021-86 (1-303) x ACA66182 (1-3716)

Qy	4	GlyGlyAspSerLeuLeuGlyGlyGlyArgGlySerLeuProLeuLeuLeuLeuMet	23
Db	1	GGAGGACGACGCTCCCTGGGGGGGAGGGGTTCCCTGCTGCTGCTGCTCATCATG	60
Qy	24	GlyGlyMetAlaGlnAspSerProGlnLeuValHisProGlnAspGlnLeuPhe	43
Db	61	GGAGGCGATGGCTCAGGACTCCCGCCCGCAGATCCTAGTCCACCCCGGACGAGCTGTC	120
Qy	44	GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProThrill	63
Db	121	CAGGGCCCTGGCCCTGCCAGGATGAGTGCCA-AGCCTCAGCCGAGCCACCTCCACCAT	179
Qy	63	eArgTrpLeuLeuAangGlyGlnProLeuSerMetValProProAspProHisHisLeuLe	83
Db	180	CCGCTGGTGTGTAATGGGACGCGCCCTGAGCATGGTGCCTCCCGCCGACACCACTTCCT	239
Qy	83	uprAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisaspGlyGly	103
Db	240	GCCTGATGGGACCTCTCTGCTGCTACAGCCCTTGGCCGGGAGCATGCCACGATGCCA	299
Qy	103	nAlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAl	123
Db	300	GGCCCTGTCCACAGACCTGGGTGTCTACATGTGAGGCCAGCAACCGCTTGGCACCGC	359
Qy	123	aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluaspGheGlnIleGlnPr	143
Db	360	AGTCAGCAGAGCGCTCGGCTGTCTGTGGCTGTCTCCGGGAGGATTTCCAGATCCAGCC	419
Qy	143	oArgAspMetValAlaValGlyGluGlnPheThrLeuGluCysGlyP-oProTrpGly	163

Db	420	TCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGATGTGGGCGCCCTGGGG	479
Qy	163	HisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGly	183
Db	480	CCACCCAGAGGCCACAGTCTCATGTGGAAGATGGGAAACCCCTGGCCCTCCAGCCCGG	539
Qy	183	YArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu**	203
Db	540	AAGGCACACAGTGTCCGGGGGTCCCTGCTGATGGCAAGACGACGAGAGAGTGACGAAGG	599
Qy	203	*-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgV	223
Db	600	-GACCTACATGTGTGTGGCCACCAACAGCGAGGACATAGGGAGAGCCGCGAGCCCGG	658
Qy	223	alSerIleGlnLupProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleG	243
Db	659	TTTCCATCCAGAGCCCGAGGACTACAGGAGCCCTGTGGAGCTTCTGGCTGGCGAATTC	718
Qy	243	InLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProA	263
Db	719	AGCTGGAAATGTGACACTGCTGAACCCGGATCTCTGCAGAGGGCCCCCAAGCCTAGACCGG	778
Qy	263	laValTrpLeu 266	
Db	779	CGGTGTGGCTC 789	

RESULT 12
AD24749
ID ADA24749 standard; cDNA; 3716 BP.
XX ADA24749;
XX 20-NOV-2003 (first entry)
XX Novel human secreted and transmembrane protein PRO860 cDNA.
XX Human; secreted and transmembrane protein; PRO; gene; ss; tissue typing;
KW Chromosome identification; vaccine; cancer; retinal disorder;
KW sports-related joint disorder; osteoarthritis; rheumatoid arthritis;
KW wound healing; obesity; diabetes; hearing loss;
KW cardiac insufficiency disorder; kidney disorder; nervous system disorder;
KW haemoglobin associated disorder.
XX Homo sapiens.
XX US2003050241-A1.
XX 13-MAR-2003.
XX 16-OCT-2001; 2001US-00978564.
XX 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066366P.
PR 11-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.

PR 30-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080328P.
PR 01-APR-1998; 98US-0080333P.
PR 01-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 09-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
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PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
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PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 22-APR-1998; 98US-0082804P.
PR 27-APR-1998; 98US-0082796P.
PR 27-APR-1998; 98US-0083336P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083392P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
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PR 29-APR-1998; 98US-0083558P.
PR 30-APR-1998; 98US-0083559P.
PR 05-MAY-1998; 98US-0083742P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 06-MAY-1998; 98US-0084416P.
PR 07-MAY-1998; 98US-0084598P.
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PR 07-MAY-1998; 98US-0084627P.
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PR 07-MAY-1998; 98US-0084643P.
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PR 15-MAY-1998; 98US-0085339P.
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PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085589P.
PR 15-MAY-1998; 98US-0085597P.
PR 15-MAY-1998; 98US-0085700P.
PR 18-MAY-1998; 98US-0085704P.
PR 22-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086332P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091339P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
PR 07-OCT-1998; 98WO-US021141.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 22-DEC-1998; 98US-0113296P.
PR 23-DEC-1998; 98US-0113621P.
PR 05-JAN-1999; 98WO-US000106.
PR 08-JAN-1999; 98WO-US005028.
PR 10-MAR-1999; 98WO-US005190.
PR 12-MAR-1999; 98US-0123957P.
PR 29-MAR-1999; 98US-0126773P.
PR 21-APR-1999; 98US-0130232P.
PR 26-APR-1999; 98US-0131022P.
PR 28-APR-1999; 98US-0131445P.
PR 14-MAY-1999; 98US-0134287P.
PR 14-MAY-1999; 98WO-US010733.
PR 02-JUN-1999; 98WO-US012252.
PR 16-JUN-1999; 98US-0139557P.
PR 23-JUN-1999; 98US-0141037P.
PR 07-JUL-1999; 98US-0142680P.
PR 26-JUL-1999; 98US-0145698P.
PR 28-JUL-1999; 98US-0146222P.
PR 29-OCT-1999; 98US-0162506P.
PR 30-NOV-1999; 98WO-US028313.
PR 02-DEC-1999; 98WO-US028551.
PR 02-DEC-1999; 98WO-US028565.
PR 16-DEC-1999; 98WO-US030095.
PR 30-DEC-1999; 98WO-US031243.
PR 30-DEC-1999; 98WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 11-FEB-2000; 2000WO-US000376.
PR 18-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015284.
PR 28-JUN-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001WO-US009552.
PR 25-MAY-2001; 2001WO-US017052.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-521814/49.
DR P-PSDB; ADA24750.
XX
XX New isolated pro polypeptides for example extracellular, secreted and
PT membrane bound proteins, useful for modulating the biological activities
PT of cells and for treating, for example diabetes, cancer, rheumatoid
PT arthritis, and hearing loss.
XX
XX Claim 2; Fig 76; 461pp; English.
XX

CC The invention describes an isolated secreted and transmembrane (PRO)
 CC polypeptide (I). PRO337 polypeptide is useful for detecting PRO4993
 CC polypeptide in a sample, and vice versa. PRO725, PRO700 and PRO739 are
 CC useful for detecting PRO1559 polypeptide in a sample, and PRO1559 is
 CC useful for detecting PRO725, PRO700 and PRO739 in a sample. PRO4993 is
 CC useful for linking a bioactive molecule to a cell expressing a PRO337
 CC polypeptide, and PRO337 is useful for linking a bioactive molecule to a
 CC cell expressing a PRO4993 polypeptide. PRO1559 is useful for linking a
 CC bioactive molecule to a cell expressing a PRO735, PRO700 and PRO739

Alignment Scores:
 Pred. No.: 1.39e-124 Length: 3716
 Score: 148.00 Matches: 261
 Percent Similarity: 98.49% Conservative: 0
 Best Local Similarity: 98.49% Mismatches: 2
 Query Match: 48.84% Indels: 4
 DB: 8 Gaps: 0

US-10-047-021-86 (1-303) x ADA24749 (1-3716)

Qy 4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuMet 23
 Db 1 GGAGGACAGACCTCTCGGGGGGAGGGGTTCTCTGCTCTGCTCTCATCATG 60
 Qy 24 GlyGlyMetAlaGlnAspSerProGlnIleuValHisProGlnAspGlnLeuPhe 43
 Db 61 GGAGGACATGGCTCAGGACTCCCGCCCGCCAGATCCTAGTCCACCCCGAGGACGCTGTTC 120
 Qy 44 GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProThrIle 63
 Db 121 CAGGGCCCTGGCCCTGCAGAGTAGCTGCCA-AGCCTCAGGCGCAGCCCTCCACCAT 179
 Qy 63 eArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisIleuLeu 83
 Db 180 CCGCTGGTTGCTGAATGGGAGAGCCCTTGAGCATGGTGGCCCGCCAGACCCACACCTCCT 239
 Qy 83 uProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGly 103
 Db 240 GCCTGATGGGACCTTCTGCTGTACAGCCCTTCCCGGGGACATGCCACCATGGCCA 299
 Qy 103 nAlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAl 123
 Db 300 GGCCCTCTCCACAGCTGGTGTCTACATGTAGGCGCAGCAACCGGCTTGGCAGCGC 359
 Qy 123 aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspGlnIleGlnPr 143
 Db 360 AGTCAGCAGAGGCGCTCGGCTGTCTGTGGTGTCTCCGGAGGATTCAGATCCAGCC 419
 Qy 143 cArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGly 163
 Db 420 TCGGGACATGGTGGCTGTGGTGGTGGAGCTTACTCTGGAATGTGGCGCGCTGGGG 479
 Qy 163 YHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGly 183
 Db 480 CCACCCAGAGCCACAGCTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCGG 539
 Qy 183 YArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu** 203
 Db 540 AAGGCACACAGTGTCCGGGGGTCCTCTGCTATGGCAAGCAGCAGAGAGTACAGAGG 599
 Qy 203 *-ThrTrpMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgV 223
 Db 600 -GACCTACATGTGTGGCCACCAACAGCGCAGGACATAGGAGAGCGCGGCGAGCCCGG 658
 Qy 223 alSerIleGlnGluProGlnAspTrpThrGluProValGluLeuLeuAlaValArgIleG 243
 Db 659 TTTCCATCCAGAGCCCGCAGGACTACAGGAGCTGTGGAGCTTCTGGCTGTGCGAATTC 718
 Qy 243 lnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProA 263
 Db 719 AGCTGGAAATGTACACTGTGTGAACCGGATCTCTGAGAGGGGCCCAAGCCCTAGACCGG 778
 Qy 263 laValTrpLeu 266

Db 779 CGGTGTGGCTC 789
 RESULT 13
 AC29783
 ID AC29783 standard; cDNA; 3716 BP.
 XX
 AC AC29783;
 XX
 DT 08-SEP-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO860 cDNA.
 XX
 KW Human; secreted and transmembrane protein; PRO; cell death; neuropathy;
 KW peripheral neuropathy; diabetic peripheral neuropathy;
 KW AIDS-associated neuropathy; Charcot-Marie-Tooth disease;
 KW Refsum's disease; Abetalipoproteinemia; Tangier disease;
 KW Krabbe's disease; Metachromatic leukodystrophy; Fabry's disease;
 KW Dejerine-Sottas syndrome; chromosome mapping; gene mapping; gene therapy;
 KW gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2003050240-A1.
 XX
 PD 13-MAR-2003.
 XX
 PF 16-OCT-2001; 2001US-00978403.
 XX
 PR 17-OCT-1997; 97US-0062250P.
 PR 13-NOV-1997; 97US-0064249P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 10-MAR-1998; 98US-0077450P.
 PR 11-MAR-1998; 98US-0077632P.
 PR 11-MAR-1998; 98US-0077641P.
 PR 11-MAR-1998; 98US-0077649P.
 PR 12-MAR-1998; 98US-0077791P.
 PR 13-MAR-1998; 98US-0078004P.
 PR 20-MAR-1998; 98US-0078888P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 20-MAR-1998; 98US-0078936P.
 PR 20-MAR-1998; 98US-0078939P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 26-MAR-1998; 98US-0079656P.
 PR 27-MAR-1998; 98US-0079663P.
 PR 27-MAR-1998; 98US-0079664P.
 PR 27-MAR-1998; 98US-0079689P.
 PR 27-MAR-1998; 98US-0079728P.
 PR 30-MAR-1998; 98US-0079786P.
 PR 30-MAR-1998; 98US-0079920P.
 PR 31-MAR-1998; 98US-0079923P.
 PR 31-MAR-1998; 98US-0080105P.
 PR 31-MAR-1998; 98US-0080107P.
 PR 31-MAR-1998; 98US-0080165P.
 PR 31-MAR-1998; 98US-0080194P.
 PR 01-APR-1998; 98US-0080327P.
 PR 01-APR-1998; 98US-0080328P.
 PR 01-APR-1998; 98US-0080333P.
 PR 01-APR-1998; 98US-0080334P.
 PR 08-APR-1998; 98US-0081049P.
 PR 08-APR-1998; 98US-0081070P.
 PR 08-APR-1998; 98US-0081071P.
 PR 09-APR-1998; 98US-0081195P.
 PR 09-APR-1998; 98US-0081203P.
 PR 09-APR-1998; 98US-0081229P.
 PR 15-APR-1998; 98US-0081817P.
 PR 15-APR-1998; 98US-0081819P.
 PR 15-APR-1998; 98US-0081838P.
 PR 15-APR-1998; 98US-0081952P.
 PR 15-APR-1998; 98US-0081955P.
 PR 21-APR-1998; 98US-0082568P.
 PR 21-APR-1998; 98US-0082569P.

Qy	24	GlyGlyMetAlaGlnAspSerProProGlnIleuValHisProGlnAspGlnLeuPhe	43	PR	17-OCT-2001;	2001US-00978824.
Db	61	GGAGGCAATGGCTCAGGACTCCCGCCCCAGATCCTAGTCCACCCCCAGGACCACTGTTTC	120	PR	21-MAY-1996;	96US-0018049P.
Qy	44	GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProThrI1	63	PR	17-OCT-1997;	97US-0062250P.
Db	121	CAGGCGCTGGCCCTGCAGGATGAGTGCCTCA-AGCTCAGGCGCAGCCACCTCCACCAT	179	PR	03-NOV-1997;	97US-0064249P.
Qy	63	eArgTTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisIleuLeu	83	PR	13-NOV-1997;	97US-0065311P.
Db	180	CCGCTGGTTCGAATGGGAGCCCTGAGCATGGTGCCTCCAGCCAGCCACCACTCCT	239	PR	21-NOV-1997;	97US-0066364P.
Qy	83	uProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyG1	103	PR	10-MAR-1998;	98US-0077450P.
Db	240	GCCTGATGGAGACCTTCGTGTGTACAGCCCTGCTCCGCGGGACATGCCACCATGGCCA	299	PR	11-MAR-1998;	98US-0077632P.
Qy	103	nAlaLeuSerThrAspLeuGlyValTyThrCysGluAlaSerAsnArgLeuGlyThrAl	123	PR	11-MAR-1998;	98US-0077641P.
Db	300	GGCCCTGTCCACAGACCTGGTGTCTACATGTAGGCGCAGCAACCGGCTTGGCAGGC	359	PR	11-MAR-1998;	98US-0077649P.
Qy	123	aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPr	143	PR	12-MAR-1998;	98US-0077791P.
Db	360	AGTCAGCAGAGGCGCTCGGCTGTCTGTGCTGTCTCCGGAGGATTTCCAGATCCAGCC	419	PR	13-MAR-1998;	98US-0078004P.
Qy	143	oArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGl	163	PR	17-MAR-1998;	98US-00040220.
Db	420	TCGGGACATGGTGTGGTGGTGGAGCATTTACTCTGGAATGTGGCGCCCTGGGG	479	PR	17-MAR-1998;	98US-0078886P.
Qy	163	yHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGl	183	PR	20-MAR-1998;	98US-0078910P.
Db	480	CCACCCAGAGCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCGG	539	PR	20-MAR-1998;	98US-0078936P.
Qy	183	yArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu**	203	PR	20-MAR-1998;	98US-0078939P.
Db	540	AGGCAACACAGTGTCCGGGGGTCTCTGCTGATGGCAAGCAGAGAGAGTGCAGAGG	599	PR	25-MAR-1998;	98US-0079294P.
Qy	203	*-ThrTyMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgV	223	PR	26-MAR-1998;	98US-0079656P.
Db	600	-GACTCATGTGTGTGGCCACCAACAGCGCAGGACATAGGAGAGCGCGCAGCCCGG	658	PR	27-MAR-1998;	98US-0079663P.
Qy	223	alSerIleGlnGluProGlnAspTyThrGluProValGluLeuAlaValArgIleG	243	PR	27-MAR-1998;	98US-0079664P.
Db	659	TTTCATCCAGAGGCCCGAGGACTACAGGAGCTGTGGAGCTTCTGGCTGTGGCAATTC	718	PR	27-MAR-1998;	98US-0079689P.
Qy	243	lnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProA	263	PR	27-MAR-1998;	98US-0079728P.
Db	719	AGCTGGAAAATGTGACACTGTGAACCCGGATCCTGCAGAGGGGCCCAAGCCTAGACCGG	778	PR	27-MAR-1998;	98US-0079788P.
Qy	263	laValTrpLeu	266	PR	30-MAR-1998;	98US-0079920P.
Db	779	CGGTGTGGCTC	789	PR	30-MAR-1998;	98US-0079923P.
RESULT 14					31-MAR-1998;	98US-0080107P.
ADAL12410					31-MAR-1998;	98US-0080165P.
ID	ADAL12410 standard; cDNA; 3716 BP.				31-MAR-1998;	98US-0080194P.
XX					31-MAR-1998;	98US-0080327P.
AC	AC ADAL12410;				01-APR-1998;	98US-0080328P.
XX					01-APR-1998;	98US-0080333P.
DT	06-NOV-2003 (first entry)				01-APR-1998;	98US-0080334P.
XX					08-APR-1998;	98US-0081071P.
XX	Human cDNA encoding secreted/transmembrane polypeptide PRO860.				08-APR-1998;	98US-0081195P.
DE					08-APR-1998;	98US-0081819P.
XX	ss; gene; inflammatory disease; organ failure; atherosclerosis;				15-APR-1998;	98US-0081838P.
KW	cardiac injury; infertility; birth defect; premature aging; AIDS; cancer;				15-APR-1998;	98US-0081952P.
KW	diabetic complication; tissue typing; human.				15-APR-1998;	98US-0081955P.
XX	Homo sapiens.				21-APR-1998;	98US-0082568P.
OS					21-APR-1998;	98US-0082569P.
FN	US2003055216-A1.				21-APR-1998;	98US-0082700P.
XX	20-MAR-2003.				22-APR-1998;	98US-0082704P.
PD					22-APR-1998;	98US-0082797P.
XX					22-APR-1998;	98US-0082804P.
XX					23-APR-1998;	98US-0082796P.
XX					23-APR-1998;	98US-0083336P.
XX					28-APR-1998;	98US-0083322P.
XX					29-APR-1998;	98US-0083495P.
XX					29-APR-1998;	98US-0083496P.
XX					29-APR-1998;	98US-0083499P.
XX					29-APR-1998;	98US-0083500P.
XX					29-APR-1998;	98US-0083545P.
XX					29-APR-1998;	98US-0083554P.
XX					29-APR-1998;	98US-0083558P.
XX					30-APR-1998;	98US-0083559P.
XX					05-MAY-1998;	98US-0083742P.
XX					06-MAY-1998;	98US-0084366P.
XX					06-MAY-1998;	98US-0084414P.
XX					07-MAY-1998;	98US-0084441P.
XX					07-MAY-1998;	98US-0084598P.
XX					07-MAY-1998;	98US-0084600P.
XX					07-MAY-1998;	98US-0084627P.
XX					07-MAY-1998;	98US-0084637P.
XX					07-MAY-1998;	98US-0084639P.
XX					07-MAY-1998;	98US-0084640P.

Db	719	AGCTGGAATGTGACACTGTGAACCCGGATCCTGCAGAGGGCCCCAAGCCTAGACCGG	778
Qy	263	lavalTrpLeu	266
Db	779	CGGRTGGCTC	789

Search completed: March 1, 2004, 07:13:32
Job time : 472 secs

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 29, 2004, 22:51:23 ; Search time 89 Seconds
(without alignments)
1889.327 Million cell updates/sec

Title: US-10-047-021-86
Perfect score: 303
Sequence: 1 MGS6GDSLLGGSGSLPLLLL.....SGPRLPREARELQGRNTG 303

Scoring table: OLIGO

Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 582709 seqs, 277475446 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1360453

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

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- 2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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c 2	8	2.6	280	4	Sequence 11, Appl
c 3	8	2.6	482	4	Sequence 278, App
4	8	2.6	571	4	US-09-016-434-278
5	8	2.6	833	2	US-09-173-151A-5
6	8	2.6	846	6	Sequence 5, Appl
7	8	2.6	993	4	US-09-621-976-264
8	8	2.6	1081	4	Sequence 264, App
9	8	2.6	1286	4	US-08-837-029-1
10	8	2.6	1339	4	US-09-615-192A-201
c 11	8	2.6	1662	4	Sequence 201, App
c 12	8	2.6	1750	4	Sequence 522, App
					Sequence 3, Appl
					Sequence 99, Appl
					Sequence 13, Appl
					Sequence 7, Appl

c 13	8	2.6	1771	3	US-08-818-112-13	Sequence 13, Appl
c 14	8	2.6	1771	4	US-08-818-111-13	Sequence 13, Appl
c 15	8	2.6	1771	4	US-09-056-556-13	Sequence 13, Appl
c 16	8	2.6	1771	4	US-09-072-596-13	Sequence 13, Appl
c 17	8	2.6	1771	4	US-09-072-967-13	Sequence 13, Appl
c 18	8	2.6	1867	1	US-07-955-905A-1	Sequence 1, Appl
c 19	8	2.6	1948	3	US-09-360-197-11	Sequence 11, Appl
c 20	8	2.6	2126	4	US-09-833-381-1979	Sequence 1979, Ap
c 21	8	2.6	2286	4	US-09-800-729-43	Sequence 43, Appl
c 22	8	2.6	2314	4	US-09-173-151A-9	Sequence 9, Appl
c 23	8	2.6	2329	4	US-09-800-729-11	Sequence 11, Appl
c 24	8	2.6	2355	4	US-09-800-729-27	Sequence 27, Appl
c 25	8	2.6	2427	4	US-09-023-655-457	Sequence 457, App
c 26	8	2.6	2480	4	US-09-202-918-1	Sequence 1, Appl
c 27	8	2.6	2635	4	US-09-673-395A-43	Sequence 43, Appl
c 28	8	2.6	2681	4	US-09-621-502-1	Sequence 1, Appl
c 29	8	2.6	2681	4	US-09-616-530A-6	Sequence 6, Appl
c 30	8	2.6	2703	4	US-09-673-395A-536	Sequence 536, App
c 31	8	2.6	2912	3	US-09-034-177-2	Sequence 2, Appl
c 32	8	2.6	2913	4	US-09-976-594-368	Sequence 368, App
c 33	8	2.6	2951	1	US-08-413-118-105	Sequence 105, App
c 34	8	2.6	2951	3	US-08-473-446-105	Sequence 105, App
c 35	8	2.6	3178	3	US-08-968-563-7	Sequence 7, Appl
c 36	8	2.6	3178	3	US-08-969-683A-7	Sequence 3, Appl
c 37	8	2.6	3178	4	US-09-297-928-3	Sequence 1, Appl
c 38	8	2.6	3215	4	US-09-719-528A-1	Sequence 2, Appl
c 39	8	2.6	3761	4	US-08-890-865A-2	Sequence 2, Appl
c 40	8	2.6	4078	4	US-09-016-434-1132	Sequence 1132, Ap
c 41	8	2.6	5690	2	US-08-447-464-2	Sequence 2, Appl
c 42	8	2.6	5690	2	US-08-718-679-2	Sequence 2, Appl
c 43	8	2.6	6000	1	US-08-348-006B-6	Sequence 6, Appl
c 44	8	2.6	6000	2	US-08-800-825A-6	Sequence 6, Appl
c 45	8	2.6	6000	3	US-09-158-657-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-10-027-983-11
; Sequence 11, Application US/10027983
; Patent No. 6617162
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Mark P. Roach
; TITLE OF INVENTION: ANTISENSE MODULATION OF ESTROGEN RECEPTOR ALPHA EXPRESSION
; FILE REFERENCE: RTS-0340
; CURRENT APPLICATION NUMBER: US/10/027,983
; CURRENT FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 11
; LENGTH: 392000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 137740
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 137742
; OTHER INFORMATION: unknown
; NAME/KEY: misc feature
; LOCATION: (138122)...(138221)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: unsure
; LOCATION: 145507
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 151967
; OTHER INFORMATION: unknown
; NAME/KEY: misc feature
; LOCATION: (151967)...(1542066)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: unsure


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RESULT 3
US-09-173-151A-5/c
; Sequence 5, Application US/09173151A
; Patent No. 6326472
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Debets, Johannes Eduard Maria
; APPLICANT: Antonius
; APPLICANT: Sana, Theodore R.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Karsleim, Robert A.
; TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/173.151A
; FILING DATE: 14-OCT-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/065,776
; FILING DATE: 17-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/078,008
; FILING DATE: 12-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/081,883
; FILING DATE: 15-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/095,987
; FILING DATE: 10-AUG-1998
; APPLICATION NUMBER: US 60/078,416
; FILING DATE: 18-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/062,065
; FILING DATE: 15-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0767X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 482 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..480
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 9
; OTHER INFORMATION: /note= "residues 9, 459, 462, 469,
; OTHER INFORMATION: and 474 each may be A, C, G, or T; translated as C "
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 246
; OTHER INFORMATION: /note= "residue 246 may be C or G;

;
; OTHER INFORMATION: translated as C"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 321
; OTHER INFORMATION: /note= "residues 321, 335, 360, and
; OTHER INFORMATION: 423 each may be C or T; translated as C"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 426
; OTHER INFORMATION: /note= "residue 426 may be A or C;
; OTHER INFORMATION: translated as C"
US-09-173-151A-5
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Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.64% Indels: 0
DB: 4 Gaps: 0
US-10-047-021-86 (1-303) x US-09-173-151A-5 (1-482)
QY 16 ProLeuLeuLeuLeuLeuLeuMet 23
DB 98 CCTCTTCGCTCTCTCTTAATG 75
RESULT 4
US-09-621-976-264
; Sequence 264, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 264
; LENGTH: 571
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 217..570
; NAME/KEY: sig_peptide
; LOCATION: 217..276
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 4.30000019073486
; OTHER INFORMATION: seq GCLLPFFVHQVG/HS
US-09-621-976-264
Alignment Scores:
Pred. No.: 126 Length: 571
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.64% Indels: 0
DB: 4 Gaps: 0
US-10-047-021-86 (1-303) x US-09-621-976-264 (1-571)
QY 14 SerLeuProLeuLeuLeuLeu 21
DB 508 TCCCTCCCTCTCTCTCTCTCTC 531
RESULT 5
US-08-837-029-1
; Sequence 1, Application US/08837029
; Patent No. 5945303
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; GENERAL INFORMATION:
; APPLICANT: Wei et al.
; TITLE OF INVENTION: Human Hematopoietic - Specific Protein
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,029
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US96/04930
; FILING DATE: 11-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 833 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 42..608
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 42..107
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 108..608
;
US-08-837-029-1
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Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.64% Indels: 0
DB: 2 Gaps: 0

US-10-047-021-86 (1-303) x US-08-837-029-1 (1-833)
Qy 14 SerLeuProLeuLeuLeuLeu 21
Db 51 TCACTGCCACTGCTGCTGCTG 74

RESULT 6
5164485-1
; Patent No. 5164485
; APPLICANT: FUJISAWA, YUKIO; ITOH, YASUAKI; NISHIMURA, OSAMU
; FUJII, TOMOKO
; TITLE OF INVENTION: MODIFIED HEPATITIS B VIRUS SURFACE
; ANTIGEN P31 AND PRODUCTION THEREOF
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/547,948
; FILING DATE: 03-JUL-1990

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 898,425
; FILING DATE: 20-AUG-1986
; SEQ ID NO: 1:
; LENGTH: 846
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5164485-1
Alignment Scores:
Pred. No.: 184 Length: 846
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.64% Indels: 0
DB: 6 Gaps: 0

US-10-047-021-86 (1-303) x 5164485-1 (1-846)
Qy 92 GlnProProAlaArgGlyHisala 99
Db 506 CAACCACCAGCACGGGGCCATGCA 529

RESULT 7
US-09-615-192A-201
; Sequence 201, Application US/09615192A
; Patent No. 6410718
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; FILE REFERENCE: 11000.1003c4U
; CURRENT APPLICATION NUMBER: US/09/615,192A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/713,000
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 201
; LENGTH: 993
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
;
US-09-615-192A-201
Alignment Scores:
Pred. No.: 214 Length: 993
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.64% Indels: 0
DB: 4 Gaps: 0

US-10-047-021-86 (1-303) x US-09-615-192A-201 (1-993)
Qy 14 SerLeuProLeuLeuLeuLeu 21
Db 53 TCCCTTCCTCTCTCTCTCTCTC 76

RESULT 8
US-09-976-594-522
; Sequence 522, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409

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; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 522
; LENGTH: 1081
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: incyte ID No. 6673549 335999.1
US-09-976-594-522

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Pred. No.: 233 Length: 1081
Score: 8.00 Matches: 8
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.64% Indels: 0
DB: 4 Gaps: 0

US-10-047-021-86 (1-303) x US-09-976-594-522 (1-1081)

Qy 14 SerLeuProLeuLeuLeuLeu 21
Db 270 TCCTTACCACCTACTACTACTACTA 293

RESULT 9
US-10-133-907-3
; Sequence 3, Application US/10133907
; Patent No. 6677369
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth R
; APPLICANT: Hoshijima, Masahiko
; TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VII
; TITLE OF INVENTION: with vesicle vector
; FILE REFERENCE: 6627-P41170
; CURRENT APPLICATION NUMBER: US/10/133,907
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/286,314
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1286
; TYPE: DNA
; ORGANISM: Hepatitis B virus
US-10-133-907-3

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Score: 8.00 Matches: 8
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.64% Indels: 0
DB: 4 Gaps: 0

US-10-047-021-86 (1-303) x US-10-133-907-3 (1-1286)

Qy 92 GlnProAlaArgGlyHisAla 99
Db 930 CAACCACACGACGCGGCCATGCA 953

RESULT 10
US-09-533-029-99
; Sequence 99, Application US/09533029
; Patent No. 6664446
; GENERAL INFORMATION:
; APPLICANT: Heard, Jacqueline
; APPLICANT: Broun, Pierre
; APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Keddie, James
; APPLICANT: Pineda, Omaira
; APPLICANT: Adam, Luc

; APPLICANT: Samaha, Raymond
; APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Reuber, Lynne
; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
; FILE REFERENCE: MBI-010
; CURRENT APPLICATION NUMBER: US/09/533,029
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 60/125,814
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 1339
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G515
US-09-533-029-99

Alignment Scores:
Pred. No.: 285 Length: 1339
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.64% Indels: 0
DB: 4 Gaps: 0

US-10-047-021-86 (1-303) x US-09-533-029-99 (1-1339)

Qy 14 SerLeuProLeuLeuLeuLeu 21
Db 611 AGCTTTCCTCTCTCTCTCTTCTT 634

RESULT 11
US-09-668-097A-13/c
; Sequence 13, Application US/09668097A
; Patent No. 6673988
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Edgar B.
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Klein, Ted
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Plant Lipases
; FILE REFERENCE: BB1401 US NA
; CURRENT APPLICATION NUMBER: US/09/668,097A
; CURRENT FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/157309
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Glycine max
US-09-668-097A-13

Alignment Scores:
Pred. No.: 351 Length: 1662
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.64% Indels: 0
DB: 4 Gaps: 0

US-10-047-021-86 (1-303) x US-09-668-097A-13 (1-1662)

Qy 15 LeuProLeuLeuLeuLeu 22
Db 664 CTACCGCTCCTCTCTCTTATTAAT 641

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.64% Indels: 0
DB: 4 Gaps: 0

US-10-047-021-86 (1-303) x US-08-818-111-13 (1-1771)

Qy 234 ProValGlulenuAlaValArg 241
Db 502 CCAAGTCGAAGTGTGGCTGTACGT 479

RESULT 15

US-09-056-556-13/C
; Sequence 13, Application US/09056556
; Patent No. 6350456
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
; NUMBER OF SEQUENCES: 241
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,556
; FILING DATE: 07-APR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.457
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1771 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-056-556-13

Alignment Scores:
Pred. No.: 373 Length: 1771
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.64% Indels: 0
DB: 4 Gaps: 0

US-10-047-021-86 (1-303) x US-09-056-556-13 (1-1771)

Qy 234 ProValGlulenuAlaValArg 241
Db 502 CCAAGTCGAAGTGTGGCTGTACGT 479

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TREATM

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Run on: March 1, 2004, 07:16:14 ; Search time 397 Seconds
(without alignments)
2753.306 Million cell updates/sec

Title: US-10-047-021-86

Perfect score: 303

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Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

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Word size: 1

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Maximum DB seq length: 2000000000

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Database : Published Applications NA:

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- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
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- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
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- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
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- 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	148	48.8	3716	9	US-09-978-697-210	Sequence 210, App
5	148	48.8	3716	9	US-09-978-192A-210	Sequence 210, App
6	148	48.8	3716	9	US-09-993-832A-210	Sequence 210, App
7	148	48.8	3716	10	US-09-978-189-210	Sequence 210, App
8	148	48.8	3716	10	US-09-978-608A-210	Sequence 210, App
9	148	48.8	3716	10	US-09-978-585A-210	Sequence 210, App
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ALIGNMENTS

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; Publication No. US20030166906A1
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; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 50 Human Secreted Proteins
; FILE REFERENCE: P2016P1
; CURRENT APPLICATION NUMBER: US/10/411,224
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/09/722,329
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/262,109
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 60/057,626
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/057,663
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; PRIOR FILING DATE: 1997-09-05
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; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,666
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: 1998-06-22
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; NAME/KEY: SITE
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; OTHER INFORMATION: n equals a,t,g, or c
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US-10-411-224-31

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Best Local Similarity: 100.00% Mismatches: 0
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; NUMBER OF SEQ ID NOS: 206
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
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US-10-411-224-31

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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.01% Indels: 0
DB: 14 Gaps: 0

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; ORGANISM: Homo sapiens
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; NAME/KEY: misc feature
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US-10-047-021-86
Alignment Scores:
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Pred. No.: 8.8e-278 Length: 1346
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Percent Similarity: 100.00% Conservatives: 0
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Db 91 CTCATCATGGAGGAGCATGGCTCAGAGCTCCCGCCCGCCAGATCTTAGTCCACCCCGAGGAC 150
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; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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Alignment Scores:

Pred. No.:	9,846-132	Length:	3716
Score:	148.00	Matches:	261
Percent Similarity:	98.49%	Conservative:	0
Best Local Similarity:	98.49%	Mismatches:	2
Query Match:	48.84%	Indels:	4
DB:	9	Gaps:	0

US-10-047-021-86 (1-303) x US-09-978-295A-210 (1-3716)

QY	4	GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuMet	23
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QY	24	GlyGlyMetAlaGlnAspSerProGlnLeuValHisProGlnAspGlnLeuPhe	43

61	GGAGGATGGCTCAGGATCCCGCGCCCGAGATCTAGTCCACCCCGAGGACAGCTGTTC	120	
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44	GinglyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProProThrI	63	
121	CAGGGCCCTGGCCCTGCCAGGATGAGTGCACA-AGCCTCAGGCAGCAGCCTCCACCAT	179	
Qy			
63	eArgTrpLeuLeuAenGlyGlnProLeuSerMetValProCaspProHisHisLeuLe	83	
180	CCGCTGGTGTCTGAATGGCGAGCCCTGAGCATGGTCCCCCAGACCCACACCACTCTCT	239	
Qy			
83	uProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyG	103	
240	GCCTGATGGGACCCCTTCTGCTGTACAGCCCTTCCCGGGGACATGCCCCAGCATGGCCA	299	
Qy			
103	nalalaSerThrAspLeuGlyValValThrCysGluAlaSerAsnArgLeuGlyThrAl	123	
300	GGCCCTGTCTCAGAGACCTGGGTGTCTACACATGTGAGCCAGCAACCGGCTTGCGCAGCG	359	
Qy			
123	aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPr	143	
360	AGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCTCCGGGAGGATTTCCAGATCCAGCC	419	
Qy			
143	oArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGl	163	
420	TCGGACACATGGTGGCTGTGGTGGGTGACAGTGTACTCTGGAATGGGGCCGCCCTGGGG	479	
Qy			
163	yHisProGluProThrValSerTrpTrpLeuAspGlyLysProLeuAlaLeuGlnProGl	183	
480	CCACCCAGAGCCACACAGTCTCATGGTGAAGATGGGAAACCCCTGGCCCTCCAGCCCGG	539	
Qy			
183	yArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu**	203	
540	AAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGACAGAGAGAGTAGTGACAGAG	599	
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203	*-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgV	223	
600	-GNCCTACATGTGTGGCCCAACACGGCAGAGCATAGGAGAGCCCGCGAGCCCGGG	658	
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223	alSerIleGlnGluProGlnIleAspTyrThrGluProValGluLeuLeuAlaValArgIleG	243	
659	TTTTCATCCAGAGAGCCCGAGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTC	718	
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243	lnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProA	263	
719	AGCTGGAAATGTGACATGTCTGAACCCGGATCTTCGACAGAGGCCCCAGCCTAGACCGG	778	
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263	laValTrpLeu 266		
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RESULT 4

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US-09-378-697-210
; Sequence 210, Application US/09378697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Garber, Hanspeter
; APPLICANT: Gillissen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Hurney, Austin L.
; APPLICANT: Hallan, Kenneth J.
; APPLICANT: Kijavani, Ivar J.
; APPLICANT: Kjug, Sophia S.

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; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	9,84e-132	Length:	3716
Score:	148.00	Matches:	261
Percent Similarity:	98.49%	Conservative:	0
Best Local Similarity:	98.49%	Mismatches:	2
Query Match:	48.84%	Indels:	4
DB:	9	Gaps:	0

US-10-047-021-86 (1-303) x US-09-978-697-210 (1-3716)

QY	4	GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuLeuMet	23
Db	1	GGAGGAGACAGCCTCTGGGGGCGAGGGTTCCCTGCTGCTGCTGCTGCTCATG	60
QY	24	GlyGlyMetAlaGlnAspSerProGlnLeuValHisProGlnAspGlnLeuPhe	43
Db	61	GGAGGATGGCTCAGGACTCCCGCCCGAGATCTGTATCCACCCCGAGGACCATGTTTC	120
QY	44	GlnGlyProGlyProAlaArgMetSerCysArg-AlaserGlyGlnProProThrIle	63
Db	121	CAGGGCCCTGGCCCTGCCAGGATGAGTGCCA-AGCCTCAGGCCAGCCACCTCCACCAT	179
QY	63	eArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisLeuLe	83
Db	180	CCGCTGGTGTGTGAATGGCGAGCCCTGAGCATGGTGGCCCGAGCCACACCATCTCT	239
QY	83	uProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyG	103
Db	240	GCTGTATGGACCCCTTCTGCTGCTACAGCCCTTCCCGGGGACATGCCACCATGCCA	299
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Qy 183 yArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu** 203
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; APPLICANT: Ashkenazi, Avi
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; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
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Alignment Scores:

Pred. No.: 9,84e-132 Length: 3716
 Score: 148.00 Matches: 261
 Percent Similarity: 98.49% Conservative: 0
 Best Local Similarity: 98.49% Mismatches: 2
 Query Match: 48.84% Indels: 4
 DB: 9 Gaps: 0

US-10-047-021-86 (1-303) x US-09-978-192A-210 (1-3716)

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 Db 240 GCCTCATGGAGCCCTTCTGCTGTACAGCCCTTCCCGGGGAGATGCCACGATGCCA 299
 QY 103 nAlaLeuSerThrAspLeuGlyValTyThrCysGlnAlaSerAsnArgLeuThrAl 123
 Db 300 GGCCCTGTCCACAGACCTGGGTGTCTACATGTAGGCCAGCAACCGCTTGGACGGC 359
 QY 123 aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPr 143
 Db 360 AGTCAGCAGAGGGCGCTCGGCTGTCTGTGGTGTCTCCCGGGAGGATTTCCAGATCCAGCC 419
 QY 143 oArgAspMetValAlaValGlyGlnGlnPheThrLeuGluCysGlyProProTrpG 163
 Db 420 TCGGGACATGGTGGTGTGGTGGGTGAGCAGTTACTCTGGAATGTGGGCGCCCTGGGG 479
 QY 163 yHisProGluProThrValSerTrpTyrAspGlyLysProLeuAlaLeuGlnProG 183
 Db 480 CCACCCAGAGCCACAGTCTCATGTGGAAGATGGGAAAACCCCTGGCCCTCCAGCCCGG 539
 QY 183 yArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu** 203
 Db 540 AAGGCACACAGTGTCCGGGGGTCTCTGCTGATGGCAAGAGCAGAGAGAGTGCAGAGG 599
 QY 203 *-ThrTy-MetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaArgV 223
 Db 600 -GACCTACATGTGTGGCCACCAACAGCGGAGGACATAGGAGAGGCCCGCCAGCCCGGG 658
 QY 223 alserIleGlnGluProGlnAspTyThrGluProValGluLeuLeuAlaValArgIleG 243
 Db 659 TTTCCATCCAGGAGGCCCCAGGACTACCGAGCCTTGTGGAGCTTCTGCTGTGGAATTC 718
 QY 243 lnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProCA 263
 Db 719 AGCTGGAAAAATGTGACACTGTGTGAACCCCGGATCTTGCAGAGGGGCCCCAAGCCTAGACCGG 778

Qy 263 laValTnpLeu 266
 Db 779 CGGTGCGCTC 789

RESULT 6
 US-09-999-832A-210
 ; Sequence 210, Application US/09999832A
 ; Publication No. US20020192706A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Flivaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
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 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2630P1C63
 ; CURRENT APPLICATION NUMBER: US/09/999,832A
 ; CURRENT FILING DATE: 2001-10-24
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/082250
 ; PRIOR FILING DATE: 1997-10-17
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 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085573
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085704
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
 Pred. No.: 9.84e-132
 Score: 148.00
 Percent Similarity: 98.49%
 Best Local Similarity: 98.49%
 Query Match: 48.84%
 DB: 9
 Length: 3716
 Matches: 261
 Conservative: 0
 Mismatches: 2
 Indels: 4
 Gaps: 0

US-10-047-021-86 (1-303) x US-09-999-832A-210 (1-3716)

Qy 4 GlyGlyaspSerLeuLeuGlyGlyargGlySerLeuProLeuLeuLeuLeuMet 23

Db 1 GGAGGAGACAGCCTCCTCGGGGGGAGGGGTTCCCTGCTCTGCTGCTCTCTCTCATCATG 60
 Qy 24 GlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
 Db 61 GGAGGACATGGCTCAGGACTCCCGGCCAGATCCTAGTCCACCCAGGACGAGTGTTC 120
 Qy 44 GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProProThrIle 63
 Db 121 CAGGGCCCTGGCCCTGCGGATGAGTGCCTA-AGCCTCAGGCGGAGCACCCTCCACCAT 179
 Qy 63 eArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLe 83
 Db 180 CGCTGGTTGCTGATGGGAGGCCCTGAGCATGGTGCCTCCACAGCCACACACCTCCT 239
 Qy 83 uProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyG 103
 Db 240 GCCTGATGGGACCTTCTGCTACAGCCCTCGCGGGGACATGCCACGATGGCCA 299
 Qy 103 nAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAl 123
 Db 300 GGCCCTGTCCACAGACCTGGGTGTCTACATGTGAGGCCAGCAACCGGCTTGACAGGC 359
 Qy 123 aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPr 143
 Db 360 AGTCAGCAGAGGCGCTCGGCTGTCTGCTGTCTCGGGGAGGATTTCCAGATCCAGCC 419
 Qy 143 oArgAspMetValAlaValValGlyGlnPheThrLeuGluCysGlyProProTrpG 163
 Db 420 TCGGGACATGGTGGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 479
 Qy 163 yHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGl 183
 Db 480 CCACCCAGAGCCACAGTCTCATGTGGAAAGATGGGAACCCCTGGCCCTCCAGCCCGG 539
 Qy 183 yArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGlyLysSerAspGlu** 203
 Db 540 AAGGCACACAGTGTCCGGGGGTCCTCTCATGTGGAGAGAGAGAGAGAGAGAGAGAG 599
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 Db 659 TTTCCATCAGAGGCGCCAGGAGTACACGAGCGCTGTGGAGCTTCTGGCTGTGGCAATTC 718
 Qy 243 InLeuGluAsnValThrLeuLeuLeuProAspProAlaGluGlyProLysProArgProA 263
 Db 719 AGCTGGAATAATGTGACACTGTGAAACCCGGATCTCTGCAGAGGGGCCCAAGCCTAGACGG 778
 Qy 263 laValTrpLeu 266
 Db 779 CGGTGTGGCTC 789

RESULT 7

US-09-978-189-210
 ; Sequence 210, Application US/09978189
 ; Publication No. US20030004102A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
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PRIOR FILING DATE: 1998-04-27
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PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06

ORGANISM: Homo sapiens
US-09-978-608A-210

Alignment Scores:
Pred. No.: 9,84e-132 Length: 3716
Score: 148.00 Matches: 261
Percent Similarity: 98.49% Conservatives: 0
Best Local Similarity: 98.49% Mismatches: 2
Query Match: 48.84% Indels: 4
DB: 10 Gaps: 0

US-10-047-021-86 (1-303) x US-09-978-608A-210 (1-3716)

Qy 4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuLeuMet 23
Db 1 GGAGGAGACAGCTCTCTGGGGGGGAGGGGTTCCTGCTGCTGCTGCTGCTCATG 60
Qy 24 GlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
Db 61 GGAGGAGATGGCTCAGGACTCTCCCGCCCGCAGATCTAGTCCACCCCGAGGACGCTGTTTC 120
Qy 44 GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProThrIle 63
Db 121 CAGGGCCCTGGCTGCGAGATGAGTGCCA-AGCCTCAGGCGCAGCAGCTCCACCAT 179
Qy 63 eArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisLeuLe 83
Db 180 CCGCTGTGTGTAATGGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 239
Qy 83 uProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisaspGlyG 103
Db 240 GCCTGATGGGACCTTCTGCTGCTACAGCCCTGCGGGGAGCATGCCACGATGCCA 299
Qy 103 nAlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAl 123
Db 300 GGCCCTGTCCACAGCTGGTGTCTACATGATGAGGCGCAGCAACCGGCTTGGCAGGC 359
Qy 123 aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPr 143
Db 360 AGTCAGCAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 419
Qy 143 oArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGl 163
Db 420 TCGGAGCATGTGGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 479
Qy 163 yHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGl 183
Db 480 CCACCCAGAGCCACAGTCTCATGTGGAAAGATGGAAACCCCTGCGCCCTCCAGCCCG 539
Qy 183 yArgHisThrValSerGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu** 203
Db 540 AAGGCACACATGTCGGGGGGGTCTCTGCTGATGGCAAGACAGAGAGAGTGCAGGAG 599
Qy 203 *ThrTyMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArg 223
Db 600 -GACCTACATGTGTGGCCCAACACAGCAGGACATAGGGAGCGCGCGCAGCCCGGG 658
Qy 223 alSerIleGlnGluProGlnAspTyThrGluProValGluLeuLeuAlaValArgIleG 243
Db 659 TTTCCATCCAGAGGCCCGCAGACTACAGGAGCCTGTGGAGCTTCTGGCTGGGAATTC 718
Qy 243 InLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProAla 263
Db 719 AGCTGGAAATGTGACATGCTGTGACCGGATCTCTGCAGAGGGGCCCAAGCCTAGACCG 778
Qy 263 lavalTrpLeu 266
Db 779 CGGTGTGGCTC 789

RESULT 9

US-09-978-585A-210
; Sequence 210, Application US/09978585A
; Publication No. US20030049633A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 210
; LENGTH: 3716
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-978-585A-210

Alignment Scores:
Pred. No.: 9,84e-132 Length: 3716
Score: 148.00 Matches: 261
Percent Similarity: 98.49% Conservatives: 0
Best Local Similarity: 98.49% Mismatches: 2
Query Match: 48.84% Indels: 4
DB: 10 Gaps: 0

US-10-047-021-86 (1-303) x US-09-978-585A-210 (1-3716)

Qy 4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuMet 23
Db 1 GGAGGAGACAGCTCTCTGGGGGGGAGGGGTTCCTGCTGCTGCTGCTCATG 60
Qy 24 GlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
Db 61 GGAGGAGATGGCTCAGGACTCTCCCGCCCGCAGATCTAGTCCACCCCGAGGACGCTGTTTC 120
Qy 44 GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProThrIle 63
Db 121 CAGGGCCCTGGCTGCGAGATGAGTGCCA-AGCCTCAGGCGCAGCAGCTCCACCAT 179
Qy 63 eArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisLeuLe 83
Db 180 CCGCTGTGTGTAATGGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 239
Qy 83 uProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisaspGlyG 103
Db 240 GCCTGATGGGACCTTCTGCTGCTACAGCCCTGCGGGGAGCATGCCACGATGCCA 299
Qy 103 nAlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAl 123

Db 300 GGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGCGCCAGCAACCGGCTTGGACAGGC 359
QY 123 aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPr 143
Db 360 AGTCAGACAGAGCGCTCGGCTGTCTGTGCTGTCTCCCGGAGGATTTCCAGATCCAGCC 419
QY 143 oArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrogI 163
Db 420 TCGGACATCGGTGGCTGTGTGGGTGAGCAGTTTACTCTGGAATGTGGGCGCCCTGGGG 479
QY 163 yHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGl 183
Db 480 CCACCCAGAGCCACAGTCTCATGTGTGGAAGATGGGAAACCCCTGGCCCTCCAGCCCGG 539
QY 183 yArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu** 203
Db 540 AAGGCACACAGTGTCCGGGGGTCCCTGCTGTGTCAGACAGACAGAGAGTGCAGAGG 599
QY 203 *-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgV 223
Db 600 -CACCTACATGTGTGTGTCACCAACAGCGGAGGACATAGGAGAGCGCGCCAGCCCGG 658
QY 223 alSerIleGlnGluProGlnAspTyrThrGluProValGluLeuAlaValArgIleG 243
Db 659 TTTCATCCAGAGAGCCCGGAGCTACACGAGCGCTGTGGAGCTTCTGGCTGTGCGAATTC 718
QY 243 InLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProA 263
Db 719 AGCTGGAATAATGTGACTGTCTGAACCCGATCTCTGCAGAGGCGCCCAAGCCTAGACCGG 778
QY 263 laValTrpLeu 266
Db 779 CGGTGTGGCTC 789

RESULT 10

US-09-978-191A-210
; Sequence 210, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.: 9,84e-132 Length: 3716
Score: 148.00 Matches: 261
Percent Similarity: 98.49% Conservativity: 0
Best Local Similarity: 98.49% Mismatches: 2
Query Match: 48.84% Indels: 4
DS: 10 Gaps: 0

US-10-047-021-86 (1-303) x US-09-978-191A-210 (1-3716)

QY 4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuLeuMet 23
DB 1 GGAGGAGACAGCTCTCTGGGGGAGGGGTTCCTGCTCTCTCTCTCTCTCATG 60
QY 24 GlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
DB 61 GGAGGATGGCTCAGGACTCCCGCCCGCCAGATCTAGTCCACCCCGAGACAGGTGTC 120
QY 44 GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProThrIle 63
DB 121 CAGGGCCCTGGCCCTGCCAGATGAGCTGCCA-AGCCTCAGCCAGCCACTCCACCAT 179
QY 63 eArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisIleLeu 83
DB 180 CCGCTGGTTGCTCATGGGAGCCCTGAGCATGGTGCCCGCCAGACCCACACCTCCT 239
QY 83 uProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyG 103
DB 240 GCCTGATGGGACCTTCTGCTGCTCAGCCCTTCCCGGGGACATGCCACATGCCA 299
QY 103 nAlaLeuSerThrAspLeuGlyValTyThrCysGluAlaSerAsnArgLeuGlyThrAl 123
DB 300 GGCCCTGTCCAGACCTGGGTGTCTACATGTGAGGCCAGCAACCGCTTGGCAGCG 359
QY 123 aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnP 143
DB 360 AGTCAGCAGAGCGCTCGGCTGTCTGTGCTCTCCCGGAGGATTCAGATCCAGCC 419
QY 143 oArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGl 163
DB 420 TCGGACATGGTGGCTGTGGTGGTGAGCAGTTACTCTGGAATGTGGCCCGCTGGGG 479
QY 163 YHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGl 183
DB 480 CCACCCAGAGCCACAGTCTCATGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCG 539
QY 183 YArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu** 203
DB 540 AAGGCACACAGTGTCCGGGGGGTCCCTGTGTGATGGCAGAGCAGACAGAGTACGAGG 599
QY 203 *-ThrTyMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgV 223
DB 600 -GACCTACATGTGTGTGGCCACCAACAGCGCAGACATAGGGAGAGCCGCGACCGCG 658
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Db 719 AGCTGAAATGTGACACTGCTGAACCCCGGATCTCTGCAGAGGGCCCCAAGGCTAGACCGG 778
QY 263 laValTriLeu 266
Db 779 CGGTGTGGCTC 789

RESULT 11
US-09-978-403A-210
; Sequence 210, Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kijavli, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C17
; CURRENT APPLICATION NUMBER: US/09/978,403A
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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 ; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
 Pred. No.: 9.84e-132
 Score: 148.00
 Percent Similarity: 98.49%
 Best Local Similarity: 98.49%

Length: 3716
 Matches: 261
 Conservative: 0
 Mismatches: 2

Query Match: 48.84% Indels: 4
 DB: 10 Gaps: 0
 US-10-047-021-86 (1-303) x US-09-978-403A-210 (1-3716)
 QY 4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuLeuMet 23
 DB 1 GGAGGAGACAGCCTCTCTGGGGGGCAGGGGTTCCCTGCCTCTGCTCTCTGCTATCATG 60
 QY 24 GlyGlyMetAlaGlnAspSerProGlnLeuValHisProGlnAspGlnLeuPhe 43
 DB 61 GGAGGCATGGCTCAGGACTCCCGGCCCCAGATCTTAGTCCACCCCCAGGACGAGTGTTC 120
 QY 44 GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProThrIle 63
 DB 121 CAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACCTCCACCACAT 179
 QY 63 eArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLe 83
 DB 180 CCGCTGGTTGCTGAATGGGCAGCCCTGAGCATGTGTGCTCCCGGAGCATGCCACGATGCCA 239
 QY 83 uProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 103
 DB 240 GCCTGATGGGACCTTCTGCTGTACAGCCCTGCCGGGGACATGCCACGATGGCCA 299
 QY 103 nAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAl 123
 DB 300 GGCCCTGTCCACAGACCTGGGGTGTCTACACATGTAGGCCAGCAACCGGCTTGGCAGCGC 359
 QY 123 aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPr 143
 DB 360 AGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCTCCGGGAGGATTTCCAGATCCAGCC 419
 QY 143 oArgAspMetValAlaValValGlyGlnPheThrLeuGluCysGlyProProTrpGln 163
 DB 420 TCGGGACATGTGTGGCTGTGTGGTGAGCAGGTTTACTCTGGAATGTGGGCCCGCCCTGGGG 479
 QY 163 yHisProGluProThrValSerTrpTyrAspGlyLysProLeuAlaLeuGlnProGln 183
 DB 480 CCACCCAGAGCCACAGTCTCATGTGTGAAGATGGGAAACCCCTGGCCCTCCAGCCCGG 539
 QY 183 yArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu** 203
 DB 540 AAGGCACACAGTGTCCGGGGGTCTCTGTGTGATGCAAGAGCAGAGAGAGTGACGAAGG 599
 QY 203 *-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgV 223
 DB 600 -GACCTACATGTGTGGCCACCAACAGCGCAGGACATAGGAGAGCGCCGAGCCCGGG 658
 QY 223 alSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleG 243
 DB 659 TTTCCATCCAGAGAGCCCGCAGGACTACACGAGCCTGTGGAGCTTCTGGCTGTGCGAAATTC 718
 QY 243 lLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProA 263
 DB 719 AGCTGGAAAATGTGACACTGCTGAACCCGGATCTCTGCAAGAGGGCCCCCAAGCCTAGACCGG 778
 QY 263 laValTrpLeu 266
 DB 779 CCGTGTGGCTC 789

RESULT 12

US-09-978-564A-210
 ; Sequence 210, Application US/09978564A
 ; Publication No. US20030050241A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
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APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC25
CURRENT APPLICATION NUMBER: US/09/978,564A
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.: 9.84e-132 Length: 3716
Score: 148.00 Matches: 261
Percent Similarity: 98.49% Conservative: 0
Best Local Similarity: 98.49% Mismatches: 2
Query Match: 48.84% Indels: 4
DB: 10 Gaps: 0

US-10-047-021-86 (1-303) x US-09-978-564A-210 (1-3716)

Qy 4 GlycylAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuMet 23
Db 1 GGAGGAGACGCTCCCTGGGGGGGAGGGTCCCTGCTGCTGCTGCTGCTCATG 60
Qy 24 GlyGlyMetAlaGlnAspSerProGlnLeuValHisProGlnAspGlnLeuPhe 43
Db 61 GGAGGAGATGCTCAGGACTCCCGCCCGCCAGATCTAGTCCACCCCGAGGACGCTGTC 120
Qy 44 GlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProThrI 63
Db 121 CAGGGCCCTGGCCCTGCGAGGATGAGTGCCA-AGCCTCAGGCCAGCCACCTCCACCAT 179
Qy 63 eArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProAspProHisLeuLe 83
Db 180 CCGTGGTGTGATGGAGCCAGCCCTGAGGATGGTGGCCCGCCAGACCCACACCTCTCT 239
Qy 83 uProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyG 103

Db 240 GCCTGATGGGACCCCTTCTGCTGTACAGCCCTCCCGGGGACATGCCCCAGATGGCCA 299
Qy 103 nAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAl 123
Db 300 GGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCAGCGC 359
Qy 123 aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPr 143
Db 360 AGTCAGCAGAGCGCTCGGCTGTCTGTGGCTGTCTCCGGGAGGATTTCCAGATCCAGCC 419
Qy 143 oArgAspMetValAlaValValGlyGluGlnPheThrLeuGlyCysGlyProProTrpGl 163
Db 420 TCGGAGCATGTGTGGTGTGGTGGTGTGTCTGTGGCTGTCTCCGGGAGGATTTCCAGATCCAGCC 479
Qy 163 yHisProGlnProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGl 183
Db 480 CCACCCAGAGCCACAGTCTCATGTGGAAAGATGGGAAACCCCTGGGCCCTCCAGCCCGG 539
Qy 183 yArgHisThrValSerGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu** 203
Db 540 AAGGCACACAGTGTCCGGGGGTCCCTGCTGATGGCAAGAGCAGAGAGAGTGCAGAAAGG 599
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Qy 223 alSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleG 243
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Qy 243 lnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProA 263
Db 719 AGCTGGAATAATGTGACACTGTCTGAACCCGGATCTCTGCAGAGGGCCCCAAGCCTAGACCGG 778
Qy 263 laValTrpLeu 266
Db 779 CCGTGTGGCTC 789

RESULT 13
US-09-999-833A-210
; Sequence 210, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
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; APPLICANT: Kuo, Sophia S.
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; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC65

1 CURRENT APPLICATION NUMBER: US/09/999,833A
2 CURRENT FILING DATE: 2001-10-24
3 PRIOR APPLICATION NUMBER: 09/918585
4 PRIOR FILING DATE: 2001-07-30
5 PRIOR APPLICATION NUMBER: 60/062250
6 PRIOR FILING DATE: 1997-10-17
7 PRIOR APPLICATION NUMBER: 60/064249
8 PRIOR FILING DATE: 1997-11-03
9 PRIOR APPLICATION NUMBER: 60/065311
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11 PRIOR APPLICATION NUMBER: 60/066364
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20 PRIOR FILING DATE: 1998-03-11
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22 PRIOR FILING DATE: 1998-03-12
23 PRIOR APPLICATION NUMBER: 60/078004
24 PRIOR FILING DATE: 1998-03-13
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143 PRIOR APPLICATION NUMBER: 60/084627
144 PRIOR FILING DATE: 1998-05-07
145 PRIOR APPLICATION NUMBER: 60/084643
146 PRIOR FILING DATE: 1998-05-07

Alignment Scores:
Pred. No.: 9,84e-132 Length: 3716
Score: 148.00 Matches: 261
Percent Similarity: 98.49% Conservative: 0
Best Local Similarity: 98.49% Mismatches: 2
Query Match: 48.84% Indels: 4
DB: 10 Gaps: 0

US-10-047-021-86 (1-303) x US-09-999-833A-210 (1-3716)

Qy 4 GlyGlyAspSerLeuLeuGlyArgGlySerLeuProLeuLeuLeuLeuMet 23
Db 1 GGAGGACACACCTCTCGGGGGGAGGGGTTCCCTGCTGCTGCTGCTCATCATG 60

Qy 24 GlyGlyMetAlaGlnAspSerProGlnLeuValHisProGlnAspGlnLeuPhe 43
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Qy 44 GlnGlyProGlyProAlaArgMetSerCysArg-AlaserGlyGlnProProThrIle 63
Db 121 CAGGCGCTGGCCCTGCGGATGAGTGCCA-AGCCTCAGGCGAGCACCTCCACCAT 179

Qy 63 eArgTrpLeuLeuGlnGlnProLeuSerMetValProProAspProHisIleLeu 83
Db 180 CCGCTGTTGCTGAATGGGAGCCCTCGAGCATGGTCCCGCCAGACCCACACCTCTCT 239

Qy 83 uProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyG1 103
Db 240 GCCTGATGGGACCTTCTGCTGCTACAGCCCTGCGGGGACATGCCAGATGGCCA 299

Qy 103 nAlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAl 123
Db 300 GGCCCTGTCCACAGCTGGGTGTCTACATGTGAGGCCAGCAACCGGCTTGGCAGGC 359

Qy 123 aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPr 143
Db 360 AGTCAGCAGAGCGCTCGGCTGTCTGGCTGCTCTCGGGAGGATTCAGATCCAGCC 419

Qy 143 oArgAspMetValAlaValGlyGluGlnPheThrLeuGluCysGlyProProThrPgl 163
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Db 540 AAGGCACACATGTTCGGGGGGTCCCTGCTGATGCGAAGAGCAGAGAGAGTACGAGG 599

Qy 203 *-ThrTyMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgv 223

Db 600 -GACCTACATGTGTGGCCACCAACAGCGAGGACATAGGAGAGCGCGAGCCCGG 658
Qy 223 alSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleG 243
Db 659 TTTCATCCAGAGAGCCCGAGGACTACAGGAGCTGTGGAGCTTCTGGCTGTGGATTC 718
Qy 243 InLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProA 263
Db 719 AGCTGGAATGTGACACTGCTGAACCGGATCTCTGCAGAGGGGCCCAAGCTAGACCG 778

Qy 263 laValTrpLeu 266
Db 779 CGGTGTGGCTC 789

RESULT 14
US-09-981-915A-210
; Sequence 210, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: P2630P1C12
; FILE REFERENCE: P2630P1C12
; CURRENT APPLICATION NUMBER: US/09/981,915A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
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; PRIOR APPLICATION NUMBER: 60/077649
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; PRIOR APPLICATION NUMBER: 60/078004

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71	PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.: 9.84e-132 Length: 3716
Score: 148.00 Matches: 261
Percent Similarity: 98.49% Conservatives: 0
Best Local Similarity: 98.49% Mismatches: 2
Query Match: 48.84% Indels: 4
DB: 10 Gaps: 0

US-10-047-021-86 (1-303) x US-09-981-915A-210 (1-3716)

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DB	1	GGAGGAGACAGCTCTCTGGGGGAGGGGTTCTCTGCTGTCTGCTCATCATG	60
QY	24	GlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPhe	43
DB	61	GGAGGCATGCTCAGGACTCCCGCCCGCCAGATCTAGTCCACCCAGGACCACTGTTTC	120
QY	44	GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProThrIle	63
DB	121	CAGGGCCCTGGCCCTGCAGAGTAGCTGCCA-AGCCTCAGGCGCCACCTCCACCAT	179
QY	63	eArgTrieLeuLeuAsnGlyGlnProLeuSerMetValProAspProHisIsteule	83
DB	180	CCGTGTGTGTGAATGGGAGCCCTTGAGCATGGTGCCTCCAGACCCACACCACTCTCT	239
QY	83	uProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisIsteule	103
DB	240	GCCTGATGGGACCTTCTGTGTACAGCCCTTGCCTGGGACATGCCACCATGGCCA	299
QY	103	nAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAl	123
DB	300	GGCCCTGTCCACAGCTGGTGTCTACATGTAGGCGCCAGCAACCGGCTGGCAGGC	359
QY	123	aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPr	143
DB	360	AGTCAGCAGAGCGCTGGCTGTCTGTGGTGTCTCTCGGGAGGATTTCCAGATCCAGCC	419
QY	143	oArgAspMetValAlaValGlyGluGlnPheThrLeuGluCysGlyProProTtpG1	163
DB	420	TCGGGACATGTGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGG	479
QY	163	yHisProGluProThrValSerTrrPlyAspGlyLeuProLeuAlaLeuGlnProG1	183
DB	480	CCACCCAGAGCCACAGCTCTCATGGTGAAAGATGGGAAACCCCTGGCCCTCCAGCCCGG	539
QY	183	yArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu**	203
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QY	223	alSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleG	243
DB	659	TTTCCATCCAGAGCCCGGAGGACTACAGGAGCTGTGGAGCTTCTGGCTGTGGCAATTC	718
QY	243	lnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProA	263
DB	719	AGCTGGAAATGTGACACTGTCTGAACCCCGGATCTCTCAGAGGGCCCCAGGCTTAGACCGG	778
QY	263	laValTrpLeu 266	
DB	779	CGGTGTGGCTC 789	

RESULT 15
US-09-978-824-210
; Sequence 210, Application US/09978824
; Publication No. US20030055216A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC14
CURRENT APPLICATION NUMBER: US/09/978,824
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	9.84e-132	Length:	3716
Score:	148.00	Matches:	261
Percent Similarity:	98.49%	Conservative:	0
Best Local Similarity:	98.49%	Mismatches:	2
Query Match:	48.84%	Indels:	4
DB:	10	Gaps:	0

US-10-047-021-86 (1-303) x US-09-978-824-210 (1-3716)

QY	4	GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuLeuMet	23
Db	1	GGAGGACAGCCCTCTGGGGGGGAGGGGTTCCTGCTGCTGCTGCTGCTCATG	60
QY	24	GlyGlyMetAlaGlnAspSerProGlnLeuValHisProGlnAspGlnLeuPhe	43
Db	61	GGAGGCATGGCTCAGGACTCCCGCCCGAGATCTCCACCCCGAGGACCACTGTC	120
QY	44	GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProThrI	63
Db	121	CAGGGCCCTGGCCCTGCCAGATGAGCTGCCA-AGCTCAGGCGCAGCCACTCCCAT	179
QY	63	eArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisLeuLe	83

Db	180	CCGCTGGTTGCTGAATGGGCAGCCCTGAGCATGGTGCCTCCGCCAGACCCACACCTCCT	239
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Db	240	GCCTGATGGGACCCCTTCTGTGCTACAGCCCCCTGCCCGGGACATGCCACCAGATGGCCA	299
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Qy	163	yHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGl	183
Db	480	CCACCCAGAGCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGGCCCTCCAGCCCGG	539
Qy	183	yArgHisThrValSerGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu**	203
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Qy	243	lnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProA	263
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Qy	263	laValTrpLeu	266
Db	779	CGGTGTGGCTC	789

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Job time : 413 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 29, 2004, 08:16:48 ; Search time 27 seconds
(without alignments)
1079.483 Million cell updates/sec

Title: US-10-047-021-86
Perfect score: 303
Sequence: 1 MGSGDLSLGGSGSLPLL.....SGPRLPEARELRQRENTG 303

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_78.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	8	2.6	72	2 AD3406	hypothetical membr
3	8	2.6	233	2 G86703	oxidoreductase YGC
4	8	2.6	431	2 T04868	hypothetical prote
5	8	2.6	437	2 S59151	NADH2 dehydrogenas
6	8	2.6	444	2 G57431	hypothetical prote
7	8	2.6	453	2 AH2649	conserved hypothet
8	8	2.6	991	2 I49540	procollagen C-endo
9	8	2.6	1102	2 JH0717	guanylate cyclase
10	8	2.6	1501	2 I58148	protein-tyrosine-p
11	8	2.6	1863	2 S46217	protein-tyrosine-p
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14	8	2.6	1898	2 S46216	leukocyte antigen-
15	8	2.6	1907	2 S50893	protein-tyrosine-p
16	8	2.6	1912	2 A56178	protein-tyrosine-p
17	8	2.6	6642	2 T29757	protein UNC-89 - C
18	7	2.3	18	2 I52614	u-plasminogen acti
19	7	2.3	24	2 I67553	monocyte chemotact
20	7	2.3	30	2 G45087	cysteine proteinas
21	7	2.3	51	2 S64676	acetylcholinestera
22	7	2.3	92	2 C75348	hypothetical prote
23	7	2.3	96	2 S31345	NADH2 dehydrogenas
24	7	2.3	100	2 S14490	ig heavy chain v r
25	7	2.3	100	2 A38685	apolipoprotein C-I
26	7	2.3	106	2 S14489	ig heavy chain v r
27	7	2.3	106	2 T06479	proline/leucine-r1
28	7	2.3	107	2 S14492	ig heavy chain v r
29	7	2.3	107	2 S14493	ig heavy chain v r

30	7	2.3	117	2 S25176	ig heavy chain v r
31	7	2.3	118	2 S24443	ig heavy chain v r
32	7	2.3	120	2 F71126	hypothetical prote
33	7	2.3	122	2 T49667	hypothetical prote
34	7	2.3	134	2 S70811	hypothetical prote
35	7	2.3	136	2 T25840	hypothetical prote
36	7	2.3	140	2 AF3282	hypothetical prote
37	7	2.3	147	2 JC7237	receptor-activity-
38	7	2.3	147	2 JC7263	receptor activity
39	7	2.3	166	2 T07089	dehydrin - soybean
40	7	2.3	184	2 S10125	alpha-2u-globulin
41	7	2.3	193	2 AF1323	3-isopropylmalate
42	7	2.3	193	2 AG1694	3-isopropylmalate
43	7	2.3	193	2 S35613	ganglioside M2 act
44	7	2.3	209	2 A54984	ELF-1 protein prec
45	7	2.3	213	2 JE0322	ephrin-A2 - human

ALIGNMENTS

RESULT 1

T42718
probable neural cell adhesion molecule L1 precursor - mouse
N;Alternate names: CHL1 protein
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 20-Jun-2000
C;Accession: T42718
R;Holm, J.; Hillenbrand, R.; Steuber, V.; Bartsch, U.; Moos, M.; Luebbert, H.; Montag, D.
submitted to the EMBL Data Library, December 1995
A;Description: Structural features of a close homolog of L1 (CHL1) in the mouse: a novel
A;Reference number: Z22239
A;Accession: T42718
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1209 <HOL>
A;Cross-references: EMBL:X94310; PIDN:CAA63972.1
A;Experimental source: brain
C;Superfamily: neural cell adhesion molecule L1; fibronectin type III repeat homology; in
C;Keywords: cell adhesion; duplication; glycoprotein; glycoprotein; transmembrane protein

Query Match 3.3%; Score 10; DB 2; Length 1209;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	116	ASNRLGTAVS	125
Db	111	ASNRLGTAVS	120

RESULT 2

AD3406
hypothetical membrane associated protein BMEI1234 [imported] - Brucella melitensis (stra
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AD3406
R;DelVecchio, V.G.; Kapratl, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P
; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis:
A;Reference number: AD3252; PMID:11756688
A;Accession: AD3406
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-72 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL52415.1; PID:GI7983217; GSPDB:GN00190
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI1234
A;Map position: 1

Query Match 2.6%; Score 8; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 4.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GSLPLLLL 20
 DB 44 GSLPLLLL 51

RESULT 3
 G97431
 C:Species: Lactococcus lactis subsp. lactis (strain IL1403)
 C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
 C:Accession: G97431
 R:Boilotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich
 Genome Res. 11, 731-753, 2001
 A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp
 A:Reference number: A86625; MUID:21235186; PMID:11337471
 A:Accession: G97431
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-233 <STO>
 A:Cross-references: GB:AB005176; PID:G12723534; PIDN:AAK04729.1; GSPDB:GN00146
 A:Experimental source: strain IL1403
 C:Genetics:
 A:Gene: y9CA

Query Match 2.6%; Score 8; DB 2; Length 233;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 QLENTVLL 250
 DB 45 QLENTVLL 52

RESULT 4
 T04868
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
 C:Accession: T04868
 R:Bevan, M.; Mueller, M.W.; Muendlein, A.; Felber, R.; Bancroft, I.; Mewes, H.W.; Mayer,
 submitted to the Protein Sequence Database, February 1999
 A:Reference number: Z15387
 A:Accession: T04868
 A:Molecule type: DNA
 A:Residues: 1-431 <BEV>
 A:Cross-references: EMBL:AL035526
 A:Experimental source: cultivar Columbia; BAC clone F28A21
 C:Genetics:
 A:Map position: 4
 A:Note: F28A21.170

Query Match 2.6%; Score 8; DB 2; Length 431;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 SLPLLLLL 21
 DB 5 SLPLLLLL 12

RESULT 5
 S59151
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 03-Jun-2002
 C:Accession: S59151
 R:Hatzoglou, E.; Rodakis, G.C.; Lecanidou, R.
 Genetics 140, 1353-1366, 1995
 A:Title: Complete sequence and gene organization of the mitochondrial genome of the land
 A:Reference number: S59143; MUID:96120351; PMID:7498775
 A:Accession: S59151

A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-437 <HAT>
 A:Cross-references: EMBL:X83390; NID:G975668; PIDN:CAAS8304.1; PID:G975677; GSPDB:GN0013;
 C:Genetics:
 A:Gene: NDA
 A:Genome: mitochondrion
 A:Genetic code: SGC4
 C:Superfamily: NADH dehydrogenase (ubiquinone) chain 4
 C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; c

Query Match 2.6%; Score 8; DB 2; Length 437;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 SLPLLLLL 21
 DB 142 SLPLLLLL 149

RESULT 6
 G97431
 C:Species: Agrobacterium tumefaciens
 C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
 C:Accession: G97431
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
 Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
 A:Reference number: A97359; MUID:21608551; PMID:11743194
 A:Accession: G97431
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-444 <KUR>
 A:Cross-references: GB:AE007869; PIDN:AAK86408.1; PID:G15155542; GSPDB:GN00169
 C:Genetics:
 A:Gene: AGR_C1055
 A:Map position: circular chromosome

Query Match 2.6%; Score 8; DB 2; Length 444;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 LLPDGTLL 89
 DB 214 LLPDGTLL 221

RESULT 7
 AH2649
 C:Species: Agrobacterium tumefaciens
 C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C:Accession: AH2649
 R:Wood, D.W.; Secubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E
 ster, E.W.
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; MUID:21608550; PMID:11743193
 A:Accession: AH2649
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-453 <KUR>
 A:Cross-references: GB:AE008688; PIDN:AAI41614.1; PID:G17738952; GSPDB:GN00186
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: Atu0597
 A:Map position: circular chromosome

Query Match 2.6%; Score 8; DB 2; Length 453;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 LLPDGTLL 89
 |||||
 Db 223 LLPDGTLL 230

RESULT 8
 149540
 collagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
 C;Accession: I49540
 R;Fukagawa, M.; Noboru, S.; Hogan, B.L.M.; Jones, C.M.
 Dev. Biol. 163, 175-183, 1994
 A;Title: Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1) which is related to the human BMP-1
 A;Reference number: I49540; MUID:94229342; PMID:8174772
 A;Accession: I49540
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-991 <RES>
 A;Cross-references: GB:I24755; NID:G439606; PIDN:AAA37306.1; PID:G439607
 C;Genetics:
 A;Gene: Bmp-1
 C;Superfamily: procollagen C-endopeptidase; astacin homology; Clr/Clis repeat homology; B
 C;Keywords: hydrolase; metalloproteinase; zinc
 F;135-326/Domain: astacin homology <AST>
 F;556-592/Domain: Clf homology <EG1>
 F;596-705/Domain: Clf/Clis repeat homology <ClR>
 F;712-747/Domain: EGF homology <EG2>
 F;218-222, 228-277/Binding site: zinc (His, His, His, Tyr) #status predicted
 F;219/Active site: Glu #status predicted

Query Match 2.6%; Score 8; DB 2; Length 991;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 SLPLLLLL 21
 |||||
 Db 13 SLPLLLLL 20

RESULT 9
 JH0717
 guanylate cyclase (EC 4.6.1.2) 2D precursor, retinal - human
 N;Alternate names: guanylyl cyclase; retinal guanylate cyclase 1
 C;Species: Homo sapiens (man)
 C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 16-Jul-1999
 C;Accession: JH0717; A55186
 R;Shyjan, A.W.; de Sauvage, F.J.; Gillett, N.A.; Goeddel, D.V.; Lowe, D.G.
 Neuron 9, 727-737, 1992
 A;Title: Molecular cloning of a retina-specific membrane guanylyl cyclase.
 A;Reference number: JH0717; MUID:93001163; PMID:I356371
 A;Accession: JH0717
 A;Molecule type: mRNA
 A;Residues: 1-1102 <SHY>
 A;Cross-references: GB:M92432
 A;Experimental source: retina
 R;Oliveira, L.; Miniou, P.; Viegas-Pequignot, E.; Rozet, J.M.; Dollfus, H.; Pittler, S.; Genomics 22, 478-481, 1994
 A;Title: Human retinal guanylate cyclase (GUC2D) maps to chromosome 17p13.1.
 A;Reference number: A55186; MUID:95104866; PMID:7806240
 A;Accession: A55186
 A;Molecule type: DNA
 A;Residues: 1001-1087 <OLI>
 A;Cross-references: GB:I26921
 C;Genetics:
 A;Gene: GDB:GUC2D
 A;Cross-references: GDB:I36012; OMIM:600179
 A;Map position: 17p13-17p13
 C;Superfamily: membrane-bound guanylate cyclase; guanylate cyclase catalytic domain hom

C;Keywords: cGMP biosynthesis; glycoprotein; phosphorus-oxygen lyase; transmembrane prote
 F;1-51/Domain: signal sequence #status predicted <SIG>
 F;52-1102/Product: guanylate cyclase #status predicted <MAT>
 F;463-487/Domain: transmembrane #status predicted <TMM>
 F;524-811/Domain: protein kinase homology <KIN>
 F;831-1059/Domain: guanylate cyclase catalytic domain homology <GCC>

Query Match 2.6%; Score 8; DB 2; Length 1102;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 LLLLOPPA 95
 |||||
 Db 42 LLLLOPPA 49

RESULT 10
 I58148
 protein-tyrosine-phosphatase (EC 3.1.3.48) 2B, splice form LAR - rat
 N;Alternate names: leukocyte common antigen-related phosphatase
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Jun-2000
 C;Accession: I58148; S46218
 R;Walton, K.M.; Martelli, K.J.; Kwak, S.P.; Dixon, J.E.; Largent, B.L.
 Neuron 11, 387-400, 1993
 A;Title: A novel receptor-type protein tyrosine phosphatase is expressed during neurogen
 A;Reference number: I58148; MUID:93357030; PMID:8352946
 A;Accession: I58148
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-1501 <WAL>
 A;Cross-references: GB:I19933; NID:G310242; PIDN:AAA42309.1; PID:G310243
 A;Note: in Genbank entry RATTYRPHOS, release 113.0, the source is designated as Rattus r
 R;Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.
 Biochem. J. 302, 39-47, 1994
 A;Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-phos
 A;Reference number: S46216; MUID:94347119; PMID:8068021
 A;Accession: S46218
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-1501 <ZHA>
 A;Cross-references: EMBL:U12329; NID:G294573; PIDN:AA37657.1; PID:G294574
 C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; :
 OGY

C;Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyrosin
 F;47-109/Domain: immunoglobulin homology <IMM1>
 F;149-209/Domain: immunoglobulin homology <IMM2>
 F;246-300/Domain: immunoglobulin homology <IMM3>
 F;413-506/Domain: fibronectin type III repeat homology <3FR>
 F;882-1501/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F;969-1190/Domain: protein-tyrosine-phosphatase homology <PTP1>
 F;1258-1481/Domain: protein-tyrosine-phosphatase homology <PTP2>
 F;1142/Active site: Cys (phosphocysteine intermediate) #link PTP1 #status predicted
 F;1148/Binding site: substrate phosphate (Arg) #link PTP1 #status predicted
 F;1433/Active site: Cys (phosphocysteine intermediate) #link PTP2 #status predicted
 F;1439/Binding site: substrate phosphate (Arg) #link PTP2 #status predicted

Query Match 2.6%; Score 8; DB 2; Length 1501;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 CVATNSAG 214
 |||||
 Db 207 CVATNSAG 214

RESULT 11
 S48217
 protein-tyrosine-phosphatase (EC 3.1.3.48) type sigma precursor - rat
 N;Alternate names: leukocyte common antigen-related phosphatase
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 07-May-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
 C;Accession: S46217; S51174; A49104

F:1544/Binding site: substrate phosphate (Arg) #status predicted
F:1829/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1835/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.6%; Score 8; DB 1; Length 1897;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 CVATNSAG 214
Db 197 CVATNSAG 204

RESULT 14
S46216
leukocyte antigen-related protein precursor - rat
N:Alternate names: leukocyte common antigen homolog
N:Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 23-Jul-1999
C/Accession: S46216; S23252; A41032; A33154
R/Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.
Biochem. J. 302, 39-47, 1994
A>Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-phosphatase
A/Reference number: S46216; MUID:94347119; PMID:8068021
A/Accession: S46216
A>Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-1898 <ZHA>
A/Cross-references: EMBL:L11586; NID:9205132; PIDN:AAAC37655.1; PID:9205133
R/Hashimoto, N.; Zhang, W.R.; Goldstein, B.J.
Biochem. J. 284, 569-576, 1992
A>Title: Insulin receptor and epidermal growth factor receptor dephosphorylation by three
A/Reference number: S23126; MUID:92287069; PMID:1599438
A/Accession: S23252
A>Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1361-1604; 1649-1898 <HAS>
R/Pot, D.A.; Woodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.E.
J. Biol. Chem. 266, 19688-19696, 1991
A>Title: Cloning, bacterial expression, purification, and characterization of the cytoplasmic
A/Reference number: A41032; MUID:92011772; PMID:1918076
A/Accession: A41032
A/Molecule type: mRNA
A/Residues: 1035-1072, 'S', 1074-1433, 'T', 1435-1638, 'N', 1640-1642, 'HT', 1645-1898 <POT>
A/Cross-references: GB:M60103; NID:9205130; PIDN:AAA41510.1; PID:9205131
R/Pot, D.A.; Woodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.E.
submitted to the Protein Sequence Database, December 1990
A/Reference number: A33154
A/Accession: A33154
A/Molecule type: mRNA
A/Residues: 1035-1072, 'S', 1074-1433, 'T', 1435-1638, 'N', 1640-1642, 'HT', 1645-1898 <PO2>
C/Comment: Only the first of the two domains homologous with protein-tyrosine-phosphatase
C/Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
ogy

C/Keywords: duplication; glycoprotein; phosphoprotein; phosphoric monoester hydrolase; tyrosine phosphatase
F:1-27/Domain: (or 1-26) signal sequence #status predicted <SIG>
F:28-1898/Product: (or 27-1898) leukocyte antigen-related protein #status predicted <MAT>
F:28-1251/Domain: (or 27-1251) extracellular #status predicted <EXT>
F:47-109/Domain: immunoglobulin homology <IMM1>
F:149-209/Domain: immunoglobulin homology <IMM2>
F:246-300/Domain: immunoglobulin homology <IMM3>
F:318-400/Domain: fibronectin type III repeat homology <FN3A>
F:413-499/Domain: fibronectin type III repeat homology <FN3B>
F:511-593/Domain: fibronectin type III repeat homology <FN3C>
F:606-695/Domain: fibronectin type III repeat homology <FN3D>
F:708-799/Domain: fibronectin type III repeat homology <FN3E>
F:811-895/Domain: fibronectin type III repeat homology <FN3F>
F:906-990/Domain: fibronectin type III repeat homology <FN3G>
F:1002-1079/Domain: fibronectin type III repeat homology <FN3H>
F:1252-1275/Domain: (or 1259-1275) transmembrane #status predicted <TM>
F:1276-1898/Domain: intracellular #status predicted <INT>
F:1286-1898/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F:1366-1597/Domain: protein-tyrosine-phosphatase homology <PTP1>
F:1655-1878/Domain: protein-tyrosine-phosphatase homology <PTP2>
F:54-107,156-207,253-298/Disulfide bonds: #status predicted
F:117,250,295,721,957/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:1539/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1545/Binding site: substrate phosphate (Arg) #status predicted
F:1830/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1836/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.6%; Score 8; DB 2; Length 1898;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 CVATNSAG 214
Db 207 CVATNSAG 214

RESULT 15
S50893
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type sigma precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 01-Aug-1995 #sequence revision 01-Sep-1995 #text_change 21-Jan-2000
C/Accession: S50893; S40281
R/Wagner, J.; Boerboom, D.; Tremblay, M.L.
Eur. J. Biochem. 226, 773-782, 1994
A>Title: Molecular cloning and tissue-specific RNA processing of a murine receptor-type I
A/Reference number: S50893; MUID:95112841; PMID:7523177
A/Accession: S50893
A>Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1907 <WAG>
A/Cross-references: EMBL:X82288; NID:9587483; PIDN:CAA57732.1; PID:9587484
R/Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
submitted to the EMBL Data Library, June 1993
A/Description: Assessment of the expression levels of murine protein-tyrosine phosphatase
A/Reference number: S40280
A/Accession: S40280
A/Molecule type: mRNA
A/Residues: 1441-1501, 'E', 1503-1546 <HEN>
A/Cross-references: EMBL:Z23050; NID:9438137; PIDN:CAA80595.1; PID:9438138
C/Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
ogy

C/Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
F:149-209/Domain: immunoglobulin homology <IMM1>
F:246-300/Domain: immunoglobulin homology <IMM2>
F:413-506/Domain: fibronectin type III repeat homology <3FR>
F:1288-1907/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:1375-1596/Domain: protein-tyrosine-phosphatase homology <PTP1>
F:1664-1887/Domain: protein-tyrosine-phosphatase homology <PTP2>
F:1548/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1554/Binding site: substrate phosphate (Arg) #status predicted
F:1839/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1845/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.6%; Score 8; DB 2; Length 1907;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 CVATNSAG 214
Db 207 CVATNSAG 214

Search completed: February 29, 2004, 08:17:50
Job time : 32 secs

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QM protein - protein search, using sw model

Run on: February 27, 2004, 17:38:30 ; Search time 19 Seconds
(without alignments)
830.382 Million cell updates/sec

Title: US-10-047-021-86
Perfect score: 303
Sequence: 1 MSGGDSLLGGRSLPLLLL.....SGPRLPREARELGRQRTNG 303

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	2.6	120	1 SV27_MOUSE	Q921X0 mus musculus
2	8	2.6	205	1 RNS9_CEBAL	Q7Y798 cebus albif
3	8	2.6	437	1 NM4M_ALRBO	P48914 albinaria c
4	8	2.6	469	1 NM01_HORSE	Q9X825 equus caball
5	8	2.6	991	1 EMPI_MOUSE	P98083 mus musculus
6	8	2.6	1103	1 CYGD_HUMAN	Q02846 homo sapien
7	8	2.6	1897	1 PTFP_HUMAN	P10586 homo sapien
8	8	2.6	1912	1 PTPD_HUMAN	P23468 homo sapien
9	8	2.6	1948	1 PTNS_HUMAN	Q13332 homo sapien
10	8	2.6	6632	1 UN89_CAEEL	C01761 caenorhabdi
11	7	2.3	96	1 NU6M_ALSTU	Q08094 albinaria t
12	7	2.3	100	1 APC2_CAVPO	P27916 cavia porce
13	7	2.3	112	1 SZ06_BOVIN	P80221 bos taurus
14	7	2.3	147	1 RMP3_MOUSE	Q9WUP1 mus musculus
15	7	2.3	148	1 RMP3_HUMAN	Q60896 homo sapien
16	7	2.3	153	1 RNS6_MOUSE	Q9D244 mus musculus
17	7	2.3	164	1 UCN3_MOUSE	Q92484 mus musculus
18	7	2.3	184	1 MUP3_MOUSE	P04939 mus musculus
19	7	2.3	184	1 RNS9_MOUSE	P60154 mus musculus
20	7	2.3	185	1 NFW_FAT	Q9K1M5 rattus norv
21	7	2.3	193	1 LEUD_LISIN	Q92A25 listeria in
22	7	2.3	193	1 LEUD_LISMO	Q8Y576 listeria mo
23	7	2.3	193	1 SAP3_MOUSE	Q60648 mus musculus
24	7	2.3	202	1 COAE_XANAC	Q9PHK7 xanthomonas
25	7	2.3	204	1 RNS9_HYLSY	Q86319 xylobates s
26	7	2.3	204	1 RNS9_PONPY	Q7YRN4 pongo pygma
27	7	2.3	205	1 BEL1_FOAMV	P14353 human spuma
28	7	2.3	205	1 RNS9_GORGO	Q863K0 gorilla gor
29	7	2.3	207	1 COAE_XANCP	Q56764 xanthomonas
30	7	2.3	209	1 EFA2_MOUSE	P52801 mus musculus
31	7	2.3	212	1 NOG2_BRARE	Q9W740 brachydanio
32	7	2.3	213	1 EFA2_HUMAN	Q43921 homo sapien
33	7	2.3	225	1 CBS1_ARCFU	Q30198 archaeoglob

ALIGNMENTS

RESULT 1

ID	SY27_MOUSE	STANDARD;	PRT;	120 AA.
AC	Q921X0; Q9DAU6; Q9DAZ4;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Small inducible cytokine A27 precursor (CC127) (CC chemokine ILC) (IL-11)			
DE	11 Ralphi-locus chemokine (mILC) (ALP) (Skinkine) (ESKine)			
DE	(Cuteaneous T-cell attracting chemokine) (CTACK).			
GN	CCL27 OR SCY27 OR ILC.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=99262167; PubMed=10329455;			
RA	Hromas R., Broxmeyer H.E., Kim C., Christopherson K. II, Hou Y.-H.;			
RT	"Isolation of ALP, a novel divergent murine CC chemokine with a unique carboxy terminal extension."			
RT	Biochem. Biophys. Res. Commun. 258:737-740(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=20026096; PubMed=10556532;			
RA	Ishikawa-Mochizuki I., Kitaura M., Baba M., Nakayama T., Izawa D.,			
RA	Imai T., Yamada H., Hieshima K., Suzuki R., Nomiya H., Yoshie O.;			
RT	"Molecular cloning of a novel CC chemokine, interleukin-11 receptor alpha-locus chemokine (ILC), which is located on chromosome 9p13 and a potential homologue of a CC chemokine encoded by molluscum contagiosum virus."			
RL	FEBS Lett. 460:544-548(1999).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=20056268; PubMed=10588729;			
RA	Morales J., Horney B., Vicari A.P., Hudak S., Oldham E., Hedrick J.,			
RA	Orozco R., Copeland N.G., Jenkins N.A., McEvoy L.M., Zlotnik A.;			
RT	"CTACK, a skin-associated chemokine that preferentially attracts skin-homing memory T cells."			
RL	Proc. Natl. Acad. Sci. U.S.A. 96:14470-14475(1999).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RC	STRAIN=C57BL/6J; TISSUE=Placenta;			
RX	MEDLINE=21085660; PubMed=11217851;			
RA	Kawai J., Shiragawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,			
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,			
RA	Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,			
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,			
RA	Kuehl P., Lewis S., Matsumoto Y., Nikaide I., Pesole G., Quackenbush J.,			
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,			
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,			
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,			
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,			

34	7	2.3	238	1	GIDB_LACLA
35	7	2.3	242	1	EPCR_MOUSE
36	7	2.3	245	1	CG21_MOUSE
37	7	2.3	246	1	CG21_HUMAN
38	7	2.3	248	1	MABC_HUMAN
39	7	2.3	249	1	YBGO_STRCO
40	7	2.3	255	1	MFA4_HUMAN
41	7	2.3	267	1	PIV6_ADE40
42	7	2.3	281	1	POTI_ECOLI
43	7	2.3	318	1	NSR_LACLA
44	7	2.3	328	1	IBP2_HUMAN
45	7	2.3	330	1	YBUX_ECOLI

Q9cfx1	lactococcus
Q64695	mus musculus
Q9jmg3	mus musculus
Q9bvt8	homo sapien
P11226	homo sapien
P40179	streptomyce
P50883	homo sapien
P48309	human adeno
P31136	escherichia
P23648	lactococcus
P18065	homo sapien
P75829	escherichia

DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00032; RNase_Pc; 1.
KW Signal.
FT CHAIN 1 24 POTENTIAL.
FT CHAIN 25 205 RIBONUCLEASE-LIKE PROTEIN 9.
FT DISULFID 97 152 BY SIMILARITY.
FT DISULFID 115 167 BY SIMILARITY.
FT DISULFID 122 129 BY SIMILARITY.
FT CARBOHYD 130 130 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 205 AA; 24294 MW; DBFC3217F7A070D0 CRC64;
Query Match 2.6%; Score 8; DB 1; Length 205;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 14 SLPLLLLL 21
Db 8 SLPLLLLL 15
RESULT 3
NU4M_ALBEO STANDARD; PRT; 437 AA.
ID NU4M_ALBEO STANDARD; PRT; 437 AA.
AC P48914;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3).
GN NU4.
OS Albinaria coerulesa (Land snail).
OG Mitochondrion.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Clausilioidae; Clausiliidae; Alopinae; Albinaria.
OX NCBI_TaxID=42349;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96120351; PubMed=7498775;
RA Hatzoglou E., Rodakis G.C., Lecanidou R.;
RT "Complete sequence and gene organization of the mitochondrial genome
of the land snail Albinaria coerulesa";
RL Genetics 140:1353-1366(1995).
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
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CC -----
DR EMBL; X83390; CAA58304.1; -.
DR PIR; S59151; S59151.
DR InterPro; IPR003918; NADHub_oxred4.
DR InterPro; IPR001750; Oxidored_q1.
DR Pfam; PF00361; oxidored_q1.
DR PRINTS; PR01437; NUOXDRDTASE4.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ SEQUENCE 437 AA; 49159 MW; 2A63927F187CA4D0 CRC64;
Query Match 2.6%; Score 8; DB 1; Length 437;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 14 SLPLLLLL 21
Db 142 SLPLLLLL 149
RESULT 4
NM01_HORSE STANDARD; PRT; 469 AA.
ID NM01_HORSE STANDARD; PRT; 469 AA.

AC Q9XSZ5;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
metalloproteinase-1) (MMP-1).
GN MMP1.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Richardson D.W.;
RT "Cloning and expression of equine matrix metalloproteinase 1
(interstitial collagenase).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cleaves collagens of types I, II, and III at one site in
the helical domain. Also cleaves collagens of types VII and X.
CC -1- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
collagen. Cleavage of the triple helix of collagen at about three-
quarters of the length of the molecule from the N-terminus, at
775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
substrates and alpha-macroglobulins at bonds where P1' is a
hydrophobic residue.
CC -1- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
similarity).
CC -1- ENZYME REGULATION: Can be activated without removal of the
activation peptide.
CC -1- SIMILARITY: Belongs to peptidase family M10A.
CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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CC -----
DR EMBL; AF148882; AAD38030.1; -.
DR HSSP; P03956; 1AYK.
DR MEROPS; M10_001; -.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR006026; Peptidase_M.
DR Pfam; PF00045; hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRININ.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
KW Hydrolase; Metalloprotease; Glycoprotein; Calcium-binding;
KW Metal-binding; Zinc; Zymogen; Collagen degradation;
KW Extracellular matrix; Signal.
FT SIGNAL 1 18 BY SIMILARITY.
FT PROPEP 19 99 ACTIVATION PEPTIDE.
FT CHAIN 100 469 INTERSTITIAL COLLAGENASE.
FT DOMAIN 215 469 HEMOPEXIN-LIKE.
FT SITE 92 92 CYSTEINE SWITCH (POTENTIAL).
FT METAL 124 124 CALCIUM 1 (BY SIMILARITY).
FT METAL 158 158 CALCIUM 2 (BY SIMILARITY).
FT METAL 168 168 ZINC 1 (BY SIMILARITY).
FT METAL 170 170 ZINC 1 (BY SIMILARITY).
FT METAL 175 175 CALCIUM 3 (BY SIMILARITY).
FT METAL 176 176 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT METAL 178 178 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT

FT METAL 180 180 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT METAL 183 183 ZINC 1 (BY SIMILARITY).
FT METAL 190 190 CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT METAL 192 192 CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT METAL 194 194 CALCIUM 2 (BY SIMILARITY).
FT METAL 196 196 ZINC 1 (BY SIMILARITY).
FT METAL 198 198 CALCIUM 3 (BY SIMILARITY).
FT METAL 199 199 CALCIUM 1 (BY SIMILARITY).
FT METAL 201 201 CALCIUM 3 (BY SIMILARITY).
FT METAL 218 218 ZINC 2 (CATALYTIC) (BY SIMILARITY).
FT ACT SITE 219 219 BY SIMILARITY.
FT METAL 222 222 ZINC 2 (CATALYTIC) (BY SIMILARITY).
FT METAL 228 228 ZINC 2 (CATALYTIC) (BY SIMILARITY).
FT METAL 285 285 CALCIUM 4 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT METAL 329 329 CALCIUM 4 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT METAL 378 378 CALCIUM 4 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT METAL 427 427 CALCIUM 4 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT DISULFID 278 466 BY SIMILARITY.
SQ SEQUENCE 469 AA; 54001 MW; ABE6760AB2C529CA CRC64;

Query Match 2.6%; Score 8; DB 1; Length 469;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 SLPLLLLL 21
DB 3 SLPLLLLL 10

RESULT 5

BMPL MOUSE STANDARD; PRT; 991 AA.
AC P98063;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Bone morphogenetic protein 1 precursor (EC 3.4.24.19) (BMP-1)
DE (Procollagen C-proteinase) (PCP) (Mammalian tolloid protein) (mtld).
GN BMPL
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6; TISSUE=Embryo;
RA MEDLINE=94223342; PubMed=8174772;
RA Fukagawa M., Nobori S., Hogan B.L.M., Jones C.M.;
RT "Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1),
RT which is related to the Drosophila dorsventral gene tolloid and
RT encodes a putative astacin metalloendopeptidase.";
RL Dev. Biol. 163:175-183(1994).
CC -!- FUNCTION: Cleaves the C-terminal propeptides of procollagen I, II
CC and III. Induces cartilage and bone formation.
CC -!- CATALYTIC ACTIVITY: Cleavage of the C-terminal propeptide at
CC Ala-I-Asp in type I and II procollagens and at Arg-I-Asp in type
CC III.
CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -!- ENZYME REGULATION: Activity is increased by the procollagen C-
CC endopeptidase enhancer protein.
CC -!- TISSUE SPECIFICITY: At high levels in embryonic maternal deciduum
CC membranous and endochondral bone, submucosa of intestine, dermis
CC of skin and the mesenchyme of spleen and lung.
CC -!- SIMILARITY: Belongs to peptidase family M12A.
CC -!- SIMILARITY: Contains 2 EGF-like domains
CC SO SEQUENCE 991 AA; 111607 MW; 68A1847783A0BB9E CRC64;

CC -!- SIMILARITY: Contains 5 CUB domains.
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CC
CC EMBL; L24755; AAA37306.1; --
CC PIR; I49540; I49540.
CC HSSP; P00736; IAPQ.
CC MEROPS; M12.005; --
CC MGD; MGI:88176; Bmp1.
CC InterPro; IPR000152; Asx hydroxyl_s.
CC InterPro; IPR000859; CUB.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR006309; EGF_Like.
CC InterPro; IPR006325; Pept_M_Zn_BS.
CC InterPro; IPR006026; Peptidase_M.
CC InterPro; IPR001506; Peptidase_M12A.
CC Pfam; PF01400; Astacin; 1.
CC Pfam; PF00431; CUB; 5.
CC Pfam; PF00008; EGF; 2.
CC PRINTS; PR00480; ASTACIN.
CC SMART; SM00042; CUB; 5.
CC SMART; SM00179; EGF_CA; 2.
CC SMART; SM00235; ZmMC; 1.
CC PROSITE; PS00010; ASX HYDROXYL; 2.
CC PROSITE; PS01180; CUB; 5.
CC PROSITE; PS00022; EGF_1; FALSE_NEG.
CC PROSITE; PS01186; EGF_2; 2.
CC PROSITE; PS00026; EGF_3; 2.
CC PROSITE; PS01187; EGF_CA; 2.
CC PROSITE; PS00142; ZINC_PROTEASE; 1.
CC KW Growth factor; Cytokine; Repeat; Osteogenesis; Chondrogenesis;
CC KW Hydrolase; Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;
CC KW Glycoprotein; Zymogen.
CC SIGNAL; 1; 25
CC PROPEP 26 125
CC CHAIN 126 991
CC DOMAIN 126 326
CC CUB 1. 327 439
CC CUB 2. 440 551
CC CUB 3. 552 593
CC CUB 4. 594 707
CC CUB 5. 708 748
CC CUB 6. 752 864
CC METAL 865 981
CC ACT SITE 218 219
CC METAL 219 219
CC METAL 222 222
CC METAL 228 228
CC DISULFID 188 191
CC DISULFID 327 353
CC DISULFID 380 402
CC DISULFID 440 466
CC DISULFID 493 515
CC DISULFID 556 568
CC DISULFID 564 577
CC DISULFID 579 592
CC DISULFID 596 622
CC DISULFID 649 671
CC DISULFID 712 723
CC DISULFID 719 732
CC DISULFID 734 747
CC CARBOHYD 96 96
CC CARBOHYD 147 147
CC CARBOHYD 337 337
CC CARBOHYD 368 368
CC CARBOHYD 604 604
CC SEQUENCE 991 AA; 111607 MW; 68A1847783A0BB9E CRC64;

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Query Match      2.6%; Score 8; DB 1; Length 991;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ov 14 SLPLLLLL 21
   |||||
Db 13 SLPLLLLL 20

RESULT 6
CYGD HUMAN
ID _CYGD HUMAN STANDARD; PRT; 1103 AA.
AC Q02846;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Retinal guanylyl cyclase 1 precursor (EC 4.6.1.2) (Guanylate cyclase
DE 2D, retinal) (RETGC-1) (Rod outer segment membrane guanylate cyclase)
DE (ROS-GC).
DE GUCY2D OR GUC2D OR RETGC1 OR RETGC OR GUC1A4 OR CORD6.
GN Homo sapiens (Human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=93001163; PubMed=1356371;
RA Shyjan A.W., de Sauvage F.J., Gillett N.A., Goeddel D.V., Lowe D.G.;
RT "Molecular cloning of a retina-specific membrane guanylyl cyclase.";
RL Neuron 9:727-737(1992).
RN [2]
RP REVISIONS.
RC TISSUE=Retina;
RA Lowe D.G.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Perrault I.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP 3D-STRUCTURE MODELING OF 871-1028.
RX MEDLINE=98054247; PubMed=9591039;
RA Liu Y., Ruocho A.E., Rao V.D., Hurley J.H.;
RT "Catalytic mechanism of the adenylyl and guanylyl cyclases: modeling
RT and mutational analysis.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:13414-13419(1997).
RN [5]
RP VARIANT LCA1 SER-52.
RX MEDLINE=97099458; PubMed=8944027;
RA Perrault I., Rozet J.M., Calvas P., Gerber S., Camuzat A.,
RA Dellifus H., Chatelin S., Souied E., Ghazi I., Leowski C.,
RA Bonnenaison M., le Paslier D., Frezal J., Dufier J.-L., Pittler S.,
RA Munnich A., Kaplan J.;
RT "Retinal-specific guanylate cyclase gene mutations in Leber's
RT congenital amaurosis.";
RL Nat. Genet. 14:461-464(1996).
RN [6]
RP VARIANT CORD6 837-ASP--MET-839.
RX MEDLINE=98349989; PubMed=9683616;
RA Perrault I., Rozet J.-M., Gerber S., Kelsell R.E., Souied E.,
RA Cabot A., Hunt D.M., Munnich A., Kaplan J.;
RT "A retGC-1 mutation in autosomal dominant cone-rod dystrophy.";
RL Am. J. Hum. Genet. 63:651-654(1998).
RN [7]
RP VARIANTS CORD6 ASP-837 AND CYS-838.
RX MEDLINE=98282246; PubMed=9618177;
RA Kelsell R.E., Gregory-Evans K., Payne A.M., Perrault I., Kaplan J.,
RA Yang R.-B., Garbers D.L., Bird A.C., Moore A.T., Hunt D.M.;
RT "Mutations in the retinal guanylate cyclase (RETGC-1) gene in dominant
RT cone-rod dystrophy.";
RL Hum. Mol. Genet. 7:1179-1184(1998).
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RN [8]
RP CHARACTERIZATION OF VARIANT SER-565.
RX MEDLINE=99105799; PubMed=9888789;
RA Duda T., Venkataraman V., Goraczniak R., Lange C., Koch K.-W.,
RA Sharma R.K.;
RT "Functional consequences of a rod outer segment membrane guanylate
RT cyclase (ROS-GC1) gene mutation linked with Leber's congenital
RT amaurosis.";
RL Biochemistry 38:509-515(1999).
RN [9]
RP VARIANTS CORD5 CYS-838 AND HIS-838.
RX MEDLINE=22439680; PubMed=12552567;
RA Udar N., Velchits S., Chalukya M., Yellore V., Nusinowitz S.,
RA Silva-Garcia R., Vrabec T., Hussles Maunee I., Donoso L.,
RA Small K.W.;
RT "Identification of GUCY2D gene mutations in CORD5 families and
RT evidence of incomplete penetrance.";
RL Hum. Mutat. 21:170-171(2003).
CC -1- FUNCTION: PROBABLY PLAYS A SPECIFIC FUNCTIONAL ROLE IN THE RODS
CC AND/OR CONES OF PHOTORECEPTORS. IT MAY BE THE ENZYME INVOLVED IN
CC THE RESYNTHESIS OF CGMP REQUIRED FOR RECOVERY OF THE DARK STATE
CC AFTER PHOTOTRANSDUCTION.
CC -1- CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphate.
CC -1- ENZYME REGULATION: Activated by GCAP-1; inhibited by calcium.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Retina. Localized exclusively in the nuclei
CC and inner segments of the rod and cone photoreceptor cells.
CC -1- DISEASE: Defects in GUCY2D are a cause of Leber congenital
CC amaurosis type 1 (LCA1) [MIM:204000]. It is characterized by total
CC blindness or greatly impaired vision with loss of central vision.
CC -1- DISEASE: Defects in GUCY2D are a cause of dominant cone-rod
CC dystrophy type 6 (CORD6) [MIM:601777]. It is characterized by the
CC initial degeneration of cone photoreceptor cells, causing early
CC loss of visual acuity and color vision, followed by the
CC degeneration of rod photoreceptor cells leading to progressive
CC night blindness and peripheral visual field loss. The disease
CC displays phenotypic heterogeneity and different gene locis are
CC involved.
CC -1- DISEASE: Defects in GUCY2D are a cause of dominant cone-rod
CC dystrophy type 5 (CORD5) [MIM:600977]. It seems to be a variant of
CC CORD6.
CC -1- SIMILARITY: Belongs to the adenylyl cyclase class-4/guanylyl
CC cyclase family.
CC -1- SIMILARITY: Contains 1 protein kinase-like domain.
CC -1- DATABASE: NAME=Mutations of the GUCY2D gene;
CC NOTE=Retina International's Scientific Newsletter;
CC WWW="http://www.retina-international.com/sci-news/gcmut.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M92432; AAA60547.1; -.
DR EMBL; AJ222657; CAA10914.1; -.
DR PIR; JH0717; JH0717.
DR PDB; 1AWL; 28-JAN-98.
DR Genew; HGNC:4689; GUCY2D.
DR MIM; 600179; -.
DR MIM; 204000; -.
DR MIM; 601777; -.
DR MIM; 600977; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005640; C:nuclear outer membrane; TAS.
DR GO; GO:0004383; F:guanylate cyclase activity; TAS.
DR GO; GO:0008075; F:receptor guanylate cyclase activity; TAS.
DR GO; GO:0007168; F:receptor guanylyl cyclase signaling pathway; TAS.
DR GO; GO:0007601; F:vision; TAS.
DR InterPro; IPR001828; ANF receptor.
DR InterPro; IPR001054; G_cyclase.
```

DR	InterPro; IPR000719; Prot kinase.	DR	DB	42 LLLQPPA 49	RESULT 7
DR	InterPro; IPR001245; Tyr_kinase.	DR	ID	PTPF HUMAN	STANDARD; PRT; 1897 AA.
DR	Pfam; PF01094; ANF_receptor; 1.	DR	AC	P10586;	
DR	Pfam; PF00211; guanylate_cyc; 1.	DR	DT	01-JUL-1989 (Rel. 11, Created)	
DR	Pfam; PF00069; Pkinase; 1.	DR	DT	01-JUL-1989 (Rel. 11, Last sequence update)	
DR	PRINTS; PR00109; TYRKINASE.	DR	DT	10-OCT-2003 (Rel. 42, Last annotation update)	
DR	ProDom; PD000001; Prot_kinase; 1.	DR	DE	LAR protein precursor (Leukocyte antigen related) (EC 3.1.3.48).	
DR	SMART; SM00044; CYCC; 1.	DR	GN	PTPRF OR LAR. (Human)	
DR	PROSITE; PS00452; GUANYLATE CYCLASES 1; 1.	DR	OS	Homo sapiens (Human)	
DR	PROSITE; PS00125; GUANYLATE CYCLASES 2; 1.	DR	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.	DR	OC	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.	
KW	Lyase; cGMP biosynthesis; Signal; Transmembrane; Vision; Glycoprotein;	DR	OX	NCBI_TaxID=9606;	
KW	Multigene family; Disease mutation; Cone-rod dystrophy; Polymorphism;	DR	ON	[1]'	
KW	3D-structure.	DR	RP	SEQUENCE FROM N.A.	
FT	SIGNAL	FT	RC	TISSUE-Tonsil.	
FT	CHAIN	FT	RC	MEDLINE=89035978; PubMed=2972792;	
FT	DOMAIN	FT	RX	Streuli M., Krueger N.X., Hall L.R., Schlossman S.F., Saito H.;	
FT	TRANSMEM	FT	RA	"A new member of the immunoglobulin superfamily that has a	
FT	DOMAIN	FT	RT	cytoplasmic region homologous to the leukocyte common antigen.";	
FT	DOMAIN	FT	RL	J. Exp. Med. 168:1523-1530(1988).	
FT	DISULFID	FT	RN	[2]	
FT	DISULFID	FT	RP	MUTAGENESIS.	
FT	CASOHYD	FT	RX	MEDLINE=90046860; PubMed=2554325;	
FT	VARIANT	FT	RA	Streuli M., Krueger N.X., Isal A.Y.M., Saito H.;	
FT	VARIANT	FT	RT	"A family of receptor-linked protein tyrosine phosphatases in humans	
FT	VARIANT	FT	RL	and Drosophila.";	
FT	VARIANT	FT	RP	Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).	
FT	VARIANT	FT	RX	[3]	
FT	VARIANT	FT	RA	MUTAGENESIS.	
FT	VARIANT	FT	RT	MEDLINE=90316093; PubMed=1695146;	
FT	VARIANT	FT	RL	Streuli M., Krueger N.X., Thal T., Tang M., Saito H.;	
FT	VARIANT	FT	RP	"Distinct functional roles of the two intracellular phosphatase like	
FT	VARIANT	FT	RX	domains of the receptor-linked protein tyrosine phosphatases LCA and	
FT	VARIANT	FT	RT	LAR.";	
FT	VARIANT	FT	RL	EMBO J. 9:2399-2407(1990).	
FT	VARIANT	FT	CC	-I- FUNCTION: It is possible that DLAR is a cell adhesion receptor.	
FT	VARIANT	FT	CC	It possesses an intrinsic protein tyrosine phosphatase activity	
FT	VARIANT	FT	CC	(PTPase).	
FT	VARIANT	FT	CC	-I- FUNCTION: The first PTPase domain has enzymatic activity, while	
FT	VARIANT	FT	CC	the second one seems to affect the substrate specificity of the	
FT	VARIANT	FT	CC	first one.	
FT	VARIANT	FT	CC	-I- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein	
FT	VARIANT	FT	CC	tyrosine + phosphate.	
FT	VARIANT	FT	CC	-I- SUBCELLULAR LOCATION: Type I membrane protein.	
FT	VARIANT	FT	CC	-I- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.	
FT	VARIANT	FT	CC	-I- SIMILARITY: Contains 8 fibronectin type III domains.	
FT	VARIANT	FT	CC	-I- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.	
FT	VARIANT	FT	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
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FT	VARIANT	FT	CC	modified and this statement is not removed. Usage by and for commercial	
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FT	VARIANT	FT	CC	or send an email to license@isb-sib.ch).	
FT	VARIANT	FT	CC	-----	
FT	VARIANT	FT	DR	EMBL; Y00815; CAA68754.1; -	
FT	VARIANT	FT	DR	FIR; S03841; TDHULK.	
FT	VARIANT	FT	DR	PDB; 1LAR; 25-APR-00.	
FT	VARIANT	FT	DR	Genew; HGNC:9670; PTPRF.	
FT	VARIANT	FT	DR	MIM; 179590; -	
FT	VARIANT	FT	DR	GO; GO:0005887; C:integral to plasma membrane; TAS.	
FT	VARIANT	FT	DR	GO; GO:0005001; P:transmembrane receptor protein tyrosine pho. . .; TAS.	
FT	VARIANT	FT	DR	GO; GO:0007155; P:cell adhesion; TAS.	
FT	VARIANT	FT	DR	GO; GO:0007185; P:transmembrane receptor protein tyrosine pho. . .; TAS.	
FT	VARIANT	FT	DR	InterPro; IPR008957; FN_III-like.	
FT	VARIANT	FT	DR	InterPro; IPR003961; FN_III.	
FT	VARIANT	FT	DR	InterPro; IPR003962; FN_III subd.	
FT	VARIANT	FT	DR	InterPro; IPR007110; Ig-like.	
FT	VARIANT	FT	DR	InterPro; IPR007110; Ig-like.	

Query Match 2.6%; Score 8; DB 1; Length 1103;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

98 LLLQPPA 95

QY


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DR InterPro; IPR003598; Ig C2.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3; 7.
DR Pfam; PF00047; ig; 3.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00014; ENTYPRIII.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 4.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS50835; IG LIKE; 3.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;
KW Cell adhesion; Immunoglobulin domain; Repeat; 3D-structure.
FT SIGNAL 1 16
FT CHAIN 17 1897
FT DOMAIN 17 1250
FT TRANSMEM 1251 1274
FT DOMAIN 1275 1897
FT DOMAIN 23 113
FT DOMAIN 125 214
FT DOMAIN 222 304
FT DOMAIN 1360 1606
FT DOMAIN 1649 1897
FT ACT_SITE 1538 1538
FT ACT_SITE 1829 1829
FT ACT_SITE 1829 1829
FT CARBOHYD 107 107
FT CARBOHYD 240 240
FT CARBOHYD 285 285
FT CARBOHYD 711 711
FT CARBOHYD 956 956
FT MUTAGEN 1538 1538
SQ SEQUENCE 1897 AA; 211844 MW; 439850F1D5C031FF CRC64;

Query Match 2.6%; Score 8; DB 1; Length 1897;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 CVATNSAG 214
|||
Db 197 CVATNSAG 204

RESULT 8
ID -PTPD_HUMAN STANDARD; PRT; 1912 AA.
AC P23458;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase delta precursor (EC 3.1.3.48) (R-PTP-
DE delta).
DE PTPD.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF ARG-1178.
RX MEDLINE=95204468; PubMed=7896816;
RA Pulido R., Krueger N.X., Serra-Pages C., Saito H., Streuli M.;
RT "Molecular characterization of the human transmembrane protein-
RT tyrosine phosphatase delta. Evidence for tissue-specific expression of
RT alternative human transmembrane protein-tyrosine phosphatase delta
RT isoforms.";
RL J. Biol. Chem. 270:6722-6728 (1995).
RN [2]
RP SEQUENCE OF 390-1912 FROM N.A.
```

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RC TISSUE=Placenta;
RX MEDLINE=91006018; PubMed=2170109;
RA Krueger N.X., Streuli M., Saito H.;
RT "Structural diversity and evolution of human receptor-like protein
RT tyrosine phosphatases";
RL EMBO J. 9:3241-3252(1990).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC IsoId=P23468-1; Sequence=Displayed;
CC Name=2; Synonyms=Kidney;
CC IsoId=P23468-2; Sequence=VSP_005147, VSP_005148, VSP_005149;
CC Name=3; Synonyms=Fetal brain;
CC IsoId=P23468-3; Sequence=VSP_005150;
CC -!- PTM: A CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN
CC FROM THE TRANSMEMBRANE SEGMENT.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 8 fibronectin type III domains.
CC -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
CC -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
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CC -----
CC EMBL; L38929; AAC41749.1; -.
CC EMBL; X54133; CAA38068.1; -.
CC PIR; A56178; A56178.
CC HSP; P18052; 1YFO.
CC Genew; HGNC:9668; PTPRD.
CC MIM; 601598; -.
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0005001; P:transmembrane receptor protein tyrosine pho. .; TAS.
CC GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
CC GO; GO:0007185; P:transmembrane receptor protein tyrosine pho. .; TAS.
CC InterPro; IPR008957; FN_III-like.
CC InterPro; IPR003961; FN_III.
CC InterPro; IPR003962; FN_III subd.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_C2.
CC InterPro; IPR00387; TYR_phosphatase.
CC InterPro; IPR000242; Tyr_PP.
CC Pfam; PF00041; fn3; 8.
CC Pfam; PF00047; ig; 3.
CC PRINTS; PR00102; Y_phosphatase; 2.
CC PRINTS; PR00014; ENTYPRIII.
CC PRINTS; PR00700; PRTYPHPTASE.
CC SMART; SM00060; FN3; 8.
CC SMART; SM00408; IGC2; 2.
CC SMART; SM00194; PTPC; 2.
CC PROSITE; PS50835; IG LIKE; 3.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
CC PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.
CC PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane; Repeat;
KW Immunoglobulin domain; Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 21 1912
FT DOMAIN 21 1265
FT TRANSMEM 1266 1290
FT DOMAIN 1291 1912
FT DOMAIN 24 114
FT DOMAIN 126 224
FT DOMAIN 236 318
FT DOMAIN 320 414
FT DOMAIN 417 513
```

FT	DOMAIN	516	606	FIBONECTIN TYPE-III 3.	RA	Danganan L., Erlar A., Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B., Arelano A., Saunders C., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S., Carrano A.V.,
FT	DOMAIN	609	708	FIBONECTIN TYPE-III 4.	RA	
FT	DOMAIN	711	822	FIBONECTIN TYPE-III 5.	RA	
FT	DOMAIN	825	916	FIBONECTIN TYPE-III 6.	RA	
FT	DOMAIN	918	1017	FIBONECTIN TYPE-III 7.	RA	
FT	DOMAIN	1020	1137	FIBONECTIN TYPE-III 8.	RT	"Sequence analysis of a 2.5 Mb region in 19p13.3";
FT	DOMAIN	1375	1618	PROTEIN-TYROSINE PHOSPHATASE 1.	RT	Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.
FT	DOMAIN	1619	1912	PROTEIN-TYROSINE PHOSPHATASE 2.	RT	
FT	ACT_SITE	1553	1553	PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY).	RP	SEQUENCE OF 1503-1589 FROM N.A.
FT	ACT_SITE	1844	1844	PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY).	RP	MEDLINE=92119637; PubMed=1370651;
FT	SITE	1175	1178	CLEAVAGE (POTENTIAL).	RA	Adachi M., Sekiya M., Arimura Y., Takekawa M., Itoh F., Hinoda Y., Imai K., Yachi A.,
FT	CARBOHYD	254	254	N-LINKED (GLCNAC. . .) (POTENTIAL).	RT	"Protein-tyrosine phosphatase expression in pre-B cell NALM-6";
FT	CARBOHYD	299	299	N-LINKED (GLCNAC. . .) (POTENTIAL).	RT	Cancer Res. 52:737-740(1992).
FT	CARBOHYD	724	724	N-LINKED (GLCNAC. . .) (POTENTIAL).	CC	-!- FUNCTION: Interacts with LAR-interacting protein LIP 1.
FT	CARBOHYD	832	832	N-LINKED (GLCNAC. . .) (POTENTIAL).	CC	-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.
FT	VARSPLIC	181	189	Missing (in isoform 2).	CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.
FT	VARSPLIC	226	229	Missing (in isoform 2).	CC	-!- ALTERNATIVE PRODUCTS:
FT	VARSPLIC	775	783	Missing (in isoform 2).	CC	Event=Alternative splicing; Named isoforms=5;
FT	VARSPLIC	609	1137	Missing (in isoform 3).	CC	Comment=Additional isoforms seem to exist;
FT	MUTAGEN	1178	1178	R->A: 2.5-FOLD REDUCTION IN CLEAVAGE.	CC	Name=PTPS;
FT	SEQUENCE	1912 AA; 214759 MW; 3A88C8CD32182E26 CRC64;			CC	Isoid=Q13332-1; Sequence=VSP_050021;
FT	SEQUENCE	2.6%; Score 8; DB 1; Length 1912;			CC	Isoid=Q13332-2; Sequence=VSP_050021;
FT	SEQUENCE	Best Local Similarity 100.0%; Pred. No. 34;			CC	Isoid=Q13332-3; Sequence=VSP_050022, VSP_050026, VSP_050027;
FT	SEQUENCE	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			CC	Name=PTPS-MEB;
QY	207 CVATNSAG 214				CC	Isoid=Q13332-4; Sequence=VSP_050024;
Db	207 CVATNSAG 214				CC	Name=PTPS-MEB;
RESULT 9					CC	Isoid=Q13332-5; Sequence=VSP_050023, VSP_050025;
PTNS HUMAN					CC	-!- TISSUE SPECIFICITY: Detected in all tissues tested except for placenta and liver.
ID	PTNS HUMAN STANDARD; PRT; 1948 AA.				CC	-!- SIMILARITY: BELONGS TO THE RECEPTOR CLASS OF THE PROTEIN-TYROSINE PHOSPHATASE FAMILY.
AC	Q13332; Q15718; Q16341;				CC	-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domain.
DT	10-OCT-2003 (Rel. 42, Created)				CC	-!- SIMILARITY: Contains 8 fibronectin type III domains.
DT	10-OCT-2003 (Rel. 42, Last sequence update)				CC	-!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
DT	10-OCT-2003 (Rel. 42, Last annotation update)				CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
DE	Receptor-type protein-tyrosine phosphatase S precursor (EC 3.1.3.48) (R-PTP-S) (Protein-tyrosine phosphatase sigma) (R-PTP-sigma).				CC	EMBL; U35234; AAC50299.1; -.
GN	PTPRS.				CC	EMBL; U40317; AAC50567.1; -.
OS	Homo sapiens (Human).				CC	EMBL; AC005790; AAC2832.1; -.
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				CC	EMBL; S78080; AAB21146.2; -.
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				CC	HSSP; P18052; LYFO.
OX	NCBI_TaxID=9606;				CC	Genew; HGNC:9681; PTPRS.
OX	[1]				CC	MIM; 601576; -.
PC	SEQUENCE FROM N.A.				CC	DR
PC	TISSUE=Fetal brain;				CC	DR
PC	MEDLINE=9610179; PubMed=8524929;				CC	DR
RA	Pulido R., Serra-Pages C., Tang M., Streuli M.;				CC	DR
RA	"The LAR/PTP delta/PTP sigma subfamily of transmembrane protein-tyrosine-phosphatases: multiple human LAR, PTP delta, and PTP sigma isoforms are expressed in a tissue-specific manner and associate with the LAR-interacting protein LIP 1."				CC	DR
RL	Proc. Natl. Acad. Sci. U.S.A. 92:11686-11690(1995).				CC	DR
RN	[2]				CC	DR
RP	SEQUENCE FROM N.A.				CC	DR
RP	MEDLINE=96255036; PubMed=8992885;				CC	DR
RA	Endo N., Rutledge S.J., Opas E.E., Vogel R., Rodan G.A., Schmidt A.;				CC	DR
RA	"Human protein tyrosine phosphatase-sigma: alternative splicing and inhibition by bisphosphonates."				CC	DR
RT	J. Bone Miner. Res. 11:535-543(1996).				CC	DR
RN	[3]				CC	DR
RP	SEQUENCE OF 1-126 FROM N.A.				CC	DR
RA	Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,				CC	DR
RA	Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,				CC	DR
RA	Phan H., Velasco N., Do L., Regalia W., Terry A., Ganes J.,				CC	DR

DR PROSITE; PS50056; TYR_PHOSPHATASE 2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;
Cell adhesion; Immunoglobulin domain; Alternative splicing; Repeat.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 1948 RECEPTOR-TYPE PROTEIN-TYROSINE
FT PHOSPHATASE S.
FT DOMAIN 30 1282 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1283 1303 POTENTIAL.
FT DOMAIN 1304 1948 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 33 123 IG-LIKE C2-TYPE 1.
FT DOMAIN 135 237 IG-LIKE C2-TYPE 2.
FT DOMAIN 245 327 IG-LIKE C2-TYPE 3.
FT DOMAIN 329 423 FIBRONECTIN TYPE-III 1.
FT DOMAIN 426 522 FIBRONECTIN TYPE-III 2.
FT DOMAIN 525 615 FIBRONECTIN TYPE-III 3.
FT DOMAIN 618 717 FIBRONECTIN TYPE-III 4.
FT DOMAIN 720 831 FIBRONECTIN TYPE-III 5.
FT DOMAIN 834 926 FIBRONECTIN TYPE-III 6.
FT DOMAIN 928 1033 FIBRONECTIN TYPE-III 7.
FT DOMAIN 1036 1151 FIBRONECTIN TYPE-III 8.
FT DOMAIN 1151 1648 PROTEIN-TYROSINE PHOSPHATASE 1.
FT DOMAIN 1648 1930 PROTEIN-TYROSINE PHOSPHATASE 2.
FT DOMAIN 641 644 POLY-PRO.
FT DISULFID 54 107 POTENTIAL.
FT DISULFID 156 216 POTENTIAL.
FT ACT_SITE 266 311 POTENTIAL.
FT ACT_SITE 1589 1589 PHOSPHOCYSTEINE INTERMEDIATE (BY
FT SIMILARITY).
FT ACT_SITE 1880 1880 PHOSPHOCYSTEINE INTERMEDIATE (BY
FT SIMILARITY).
FT CARBOHYD 263 263 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 308 308 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 733 733 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 940 940 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARSPLIC 190 198 Missing (in isoform PTPS-MEA).
FT VARSPLIC 236 239 /FtId=VSP_050021.
FT VARSPLIC 617 1034 /FtId=VSP_050022.
FT VARSPLIC 784 792 /FtId=VSP_050023.
FT VARSPLIC 1035 1035 /FtId=VSP_050024.
FT VARSPLIC 1350 1365 V -> I (in isoform PTPS-F4-7).
FT VARSPLIC 1366 1366 Missing (in isoform PTPS-MEB).
FT VARSPLIC 310 310 S -> G (in isoform PTPS-MEB).
FT VARSPLIC 428 429 T -> HP (in isoform PTPS-MEB).
FT VARSPLIC 742 745 LGPV -> RSPA (in isoform PTPS-F4-7).
FT VARSPLIC 765 773 GAERGPPR -> RREARRRS (in isoform PTPS-F4-7).
FT VARSPLIC 910 910 R -> P (in isoform PTPS-F4-7).
FT VARSPLIC 986 995 AAEPGAENAV -> GRLSRRRTL (in isoform PTPS-F4-7).
FT VARSPLIC 1195 1196 TV -> SL (in isoform PTPS-F4-7).
FT VARSPLIC 1431 1431 F -> S (in isoform PTPS-F4-7).
FT VARSPLIC 1546 1546 E -> D (in isoform PTPS-F4-7).
FT VARSPLIC 1587 1587 V -> A (in isoform PTPS-F4-7).
FT VARSPLIC 1705 1705 N -> K (in isoform PTPS-F4-7).
SQ SEQUENCE 1948 AA; 217080 NW; 7DC049EC03171136 CRC64;
Query Match 2.6%; Score 8; DB 1; Length 1948;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 207 CVATNSAG 214
Db 216 CVATNSAG 223
RESULT 10
UN89_CABEL

ID UN89_CABEL STANDARD; PRT; 6632 AA.
AC 001761; 017362;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE Muscle M-line assembly protein unc-89 (Uncoordinated protein 89).
GN UNC-89 OR C09D1.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC STRAIN=Bristol N2;
RX MEDLINE=96180278; PubMed=8603916;
RA Benian G.M., Tinley T.L., Tang X., Borodovsky M.;
RT "The Caenorhabditis elegans gene unc-89, required for muscle M-line
transduction domains.";
RL J. Cell Biol. 132:835-848(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Du Z., Le T.T., Wilson R.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP REVISIONS.
RA Waterston R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Structural component of the muscle M-line. Myofibrillar
lattice assembly begins with positional cues laid down in the
basement membrane and muscle cell membrane. UNC-89 responds to
these signals, localizes, and then participates in assembling an
M-line.
CC -!- TISSUE SPECIFICITY: Localizes to the middle of A-bands.
CC -!- SIMILARITY: Contains 1 DBL-homology (DH) domain.
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
CC -!- SIMILARITY: Contains 49 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 1 PH domain.
CC -!- SIMILARITY: Contains 5 RCD domains.
CC -!- SIMILARITY: Contains 1 SH3 domain.
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
EMBL; U33058; AAB00542.1; -
EMBL; AF003131; AAB54132.2; -
PDB; 1FHO; 20-DEC-00.
WormPep; C09D1.1; CE30426.
InterPro; IPR008957; FN.III-like.
InterPro; IPR003961; FN.III.
InterPro; IPR007110; IG-like.
InterPro; IPR003598; IG_C2.
InterPro; IPR003006; IG_MHC.
InterPro; IPR001849; PH.
InterPro; IPR007850; RCD.
InterPro; IPR000219; RhoGEF.
InterPro; IPR001452; SH3.
Pfam; PF00041; fn3; 1.
Pfam; PF00047; ig; 47.
Pfam; PF00169; PH; 1.
Pfam; PF05177; RCD; 5.
Pfam; PF00621; RhoGEF; 1.
Pfam; PF00018; SH3; 1.
SMART; SM00408; IGC2; 23.
SMART; SM00325; RhoGEF; 1.
SMART; SM00326; SH3; 1.
PROSITE; PS50010; DH_2; 1.

DR PROSITE; PS50835; IG LIKE; 49.
 DR PROSITE; PS50003; PH DOMAIN; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW Muscle protein; Immunoglobulin domain; Repeat; SH3 domain;
 3D-structure.

FT	DOMAIN	63	127	SH3.
FT	DOMAIN	152	330	DH.
FT	DOMAIN	342	498	PH.
FT	DOMAIN	547	633	IG-LIKE C2-TYPE 1.
FT	DOMAIN	648	736	IG-LIKE C2-TYPE 2.
FT	DOMAIN	748	838	IG-LIKE C2-TYPE 3.
FT	DOMAIN	946	1033	IG-LIKE C2-TYPE 4.
FT	DOMAIN	1044	1132	IG-LIKE C2-TYPE 5.
FT	DOMAIN	1140	1227	IG-LIKE C2-TYPE 6.
FT	DOMAIN	1375	1415	THR-RICH.
FT	DOMAIN	1372	1475	RCSD 1.
FT	DOMAIN	1479	1585	RCSD 2.
FT	DOMAIN	1597	1695	RCSD 3.
FT	DOMAIN	1700	1799	RCSD 4.
FT	DOMAIN	1800	1860	RCSD 5.
FT	DOMAIN	1982	2067	IG-LIKE C2-TYPE 7.
FT	DOMAIN	2071	2163	IG-LIKE C2-TYPE 8.
FT	DOMAIN	2171	2261	IG-LIKE C2-TYPE 9.
FT	DOMAIN	2269	2359	IG-LIKE C2-TYPE 10.
FT	DOMAIN	2367	2455	IG-LIKE C2-TYPE 11.
FT	DOMAIN	2463	2564	IG-LIKE C2-TYPE 12.
FT	DOMAIN	2563	2651	IG-LIKE C2-TYPE 13.
FT	DOMAIN	2657	2746	IG-LIKE C2-TYPE 14.
FT	DOMAIN	2754	2858	IG-LIKE C2-TYPE 15.
FT	DOMAIN	2887	2980	IG-LIKE C2-TYPE 16.
FT	DOMAIN	2994	3081	IG-LIKE C2-TYPE 17.
FT	DOMAIN	3087	3183	IG-LIKE C2-TYPE 18.
FT	DOMAIN	3189	3280	IG-LIKE C2-TYPE 19.
FT	DOMAIN	3286	3376	IG-LIKE C2-TYPE 20.
FT	DOMAIN	3384	3469	IG-LIKE C2-TYPE 21.
FT	DOMAIN	3482	3572	IG-LIKE C2-TYPE 22.
FT	DOMAIN	3580	3667	IG-LIKE C2-TYPE 23.
FT	DOMAIN	3686	3777	IG-LIKE C2-TYPE 24.
FT	DOMAIN	3817	3908	IG-LIKE C2-TYPE 25.
FT	DOMAIN	3920	4009	IG-LIKE C2-TYPE 26.
FT	DOMAIN	4018	4106	IG-LIKE C2-TYPE 27.
FT	DOMAIN	4109	4201	IG-LIKE C2-TYPE 28.
FT	DOMAIN	4212	4297	IG-LIKE C2-TYPE 29.
FT	DOMAIN	4302	4387	IG-LIKE C2-TYPE 30.
FT	DOMAIN	4400	4485	IG-LIKE C2-TYPE 31.
FT	DOMAIN	4489	4580	IG-LIKE C2-TYPE 32.
FT	DOMAIN	4588	4678	IG-LIKE C2-TYPE 33.
FT	DOMAIN	4681	4771	IG-LIKE C2-TYPE 34.
FT	DOMAIN	4873	4961	IG-LIKE C2-TYPE 35.
FT	DOMAIN	4965	5057	IG-LIKE C2-TYPE 36.
FT	DOMAIN	5067	5160	IG-LIKE C2-TYPE 37.
FT	DOMAIN	5171	5260	IG-LIKE C2-TYPE 38.
FT	DOMAIN	5277	5366	IG-LIKE C2-TYPE 39.
FT	DOMAIN	5383	5472	IG-LIKE C2-TYPE 40.
FT	DOMAIN	5487	5578	IG-LIKE C2-TYPE 41.
FT	DOMAIN	5595	5685	IG-LIKE C2-TYPE 42.
FT	DOMAIN	5701	5790	IG-LIKE C2-TYPE 43.
FT	DOMAIN	5815	5904	IG-LIKE C2-TYPE 44.
FT	DOMAIN	5925	6014	IG-LIKE C2-TYPE 45.
FT	DOMAIN	6038	6130	IG-LIKE C2-TYPE 46.
FT	DOMAIN	6150	6239	IG-LIKE C2-TYPE 47.
FT	DOMAIN	6275	6368	FIBRONECTIN TYPE-III.
FT	DOMAIN	6413	6502	IG-LIKE C2-TYPE 48.
FT	DOMAIN	6507	6596	IG-LIKE C2-TYPE 49.
FT	DOMAIN	568	621	POTENTIAL.
FT	DISULFID	2308	2975	POTENTIAL.
FT	DISULFID	3015	3065	POTENTIAL.
FT	DISULFID	3707	3759	POTENTIAL.
FT	DISULFID	3826	3890	POTENTIAL.
FT	DISULFID	5092	5157	POTENTIAL.
FT	DISULFID	5298	5350	POTENTIAL.
FT	DISULFID	5508	5560	POTENTIAL.
FT	DISULFID	5616	5669	POTENTIAL.

Query Match 2.6%; Score 8; DB 1; Length 6632;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 WLLNGQPL 72
 |||||
 DB 2205 WLLNGQPL 2212

RESULT 11
 NU6M ALBTU STANDARD; PRT; 96 AA.
 AC Q08084;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DE 01-FEB-1996 (Rel. 33, Last annotation update)
 DE NADH-ubiquinone oxidoreductase chain 6 (EC 1.6.5.3) (Fragment).
 GN ND6.
 OS Albinaria turrita (Door snail).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 OC Sigmurethra; clausilidae; Clausiliidae; Alopinae; Albinaria.
 OC NCBI_TaxID=27820;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94275981; PubMed=8007005;
 RA Lecanidou R., Douris V., Rodakis G.C.;
 RT "Novel features of metazoan mtDNA revealed from sequence analysis of
 three mitochondrial DNA segments of the land snail Albinaria turrita
 (Gastropoda: Clausiliidae).";
 RL J. Mol. Evol. 38:369-382(1994).
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
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EMBL; X71394; CAA50516.1; -
 DR PIR; S33145; S33145.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
 FT NON_TER 96
 SQ SEQUENCE 96 AA; 10896 MW; A1732AACCA4FADA4F CRC64;

Query Match 2.3%; Score 7; DB 1; Length 96;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
 RN NCBI_TaxID=10090;

[1]

RP SEQUENCE FROM N.A.
 RA Derst C., Preisig-Mueller R., Gerhard J., Daut J.;
 RT "Cloning and sequencing of mouse CGRP/adrenomedullin receptor
 subunits";

RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.

[2]

RN SEQUENCE FROM N.A.

RA Husmann K., Sexton P.M., Fischer J.A., Born W.;

RT "Mouse receptor activity modifying proteins 1, -2 and -3: amino acid

sequence, expression and function";

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

[3]

RN SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Lung;

RA Ono Y., Okano I., Kojima M., Okada K., Kangawa K.;

RT "cDNA cloning of mouse CRLR and RAMPs";

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

[4]

RN SEQUENCE FROM N.A.

RP TISSUE=Eye;

RX MEDLINE=22389257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Blakesley R.W., Touchman J.W., Green E.D., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC -!- FUNCTION: Required to transport calcitonin-receptor-like receptor

(CRLR) to the plasma membrane (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -!- SIMILARITY: Belongs to the RAMP family.

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 or send an email to license@isb-sib.ch).

CC EMBL; AF146524; AAD35020.1; -

DR EMBL; AF250491; CAB59513.1; -

DR EMBL; AF209907; AAF21039.1; -

DR EMBL; BC024765; AAB24765.1; -

DR MGP; WGI-1860292; RAMP3

DR GO; GO:0015027; F:coreceptor, soluble ligand activity; IDA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IPI.

DR InterPro; IPR006985; RAMP.

DR Pfam; PF04901; RAMP; 1.

DR Signal; Transmembrane; Transport; Receptor.

FT SIGNAL 1 22 POTENTIAL.

FT CHAIN 23 147 RECEPTOR ACTIVITY-MODIFYING PROTEIN 3.

FT DOMAIN 23 117 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 118 137 POTENTIAL.

FT DOMAIN 138 147 CYTOPLASMIC (POTENTIAL).

SQ SEQUENCE 147 AA; 16779 MW; 359EE741034C34E8 CRC64;

Query Match 2.3%; Score 7; DB 1; Length 147;

Best Local Similarity 100.0%; Pred. No. 32;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 15 LPLLLLL 21

Db 11 LPLLLLL 17

RESULT 15

RMP3 HUMAN

ID_RMP3_HUMAN STANDARD; PRT; 148 AA.

AC 060896;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Receptor activity-modifying protein 3 precursor (CRLR activity-

DE modifying-protein 3) (Calcitonin-receptor-like receptor-activity-

DE modifying-protein 3).

GN RAMP3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1] SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.

RP TISSUE=Brain;

RX MEDLINE=98282119; PubMed=9620797;

RA McLatchie L.M., Fraser N.J., Main M.J., Wise A., Brown J.,

RA Thompson N., Solari R., Lee M.G., Foord S.M.;

RT "RAMPs regulate the transport and ligand specificity of the

calcitonin-receptor-like receptor";

RT Nature 393:333-339 (1998).

RN [2] SEQUENCE FROM N.A.

RP Kopatz S.A., Aronstam R.S., Sharma S.V.;

RT "cDNA clones of human proteins involved in signal transduction

sequenced by the Guthrie cDNA resource center (www.cdna.org).";

RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

RN [3] SEQUENCE FROM N.A.

RP TISSUE=Lung;

RX MEDLINE=22389257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Blakesley R.W., Touchman J.W., Green E.D., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [4]

RP SEQUENCE OF 21-148 FROM N.A.

RA Walker C., Bauer C., Smith R.;

RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Required to transport calcitonin-receptor-like receptor

(CRLR) to the plasma membrane.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: Strongly expressed in lung, breast, immune

```

CC      system and fetal tissues.
CC      -!- SIMILARITY: Belongs to the RAMP family.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; AJ001016; CAA0474.1; -
CC      EMBL; AY265459; AAP23300.1; -
CC      EMBL; BC022304; AAH22304.1; -
CC      EMBL; AC004844; -; NOT_ANNOTATED_CDS.
CC      Genew; HGNC:9845; RAMP3.
CC      MIN; 605155; -
CC      DR GO; GO:0005887; C:integral to plasma membrane; TAS.
CC      DR GO; GO:0005764; C:lysosome; TAS.
CC      DR GO; GO:0015031; P:protein transport; TAS.
CC      DR GO; GO:0006898; P:receptor mediated endocytosis; TAS.
CC      DR InterPro; IPR006985; RAMP.
CC      Pfam; PF04901; RAMP; 1.
CC      KX Signal; Transmembrane; Transport; Receptor.
CC      FT SIGNAL 1 23 POTENTIAL.
CC      FT CHAIN 24 148 RECEPTOR ACTIVITY-MODIFYING PROTEIN 3.
CC      FT DOMAIN 24 118 EXTRACELLULAR (POTENTIAL).
CC      FT TRANSMEM 119 138 POTENTIAL.
CC      FT DOMAIN 139 148 CYTOPLASMIC (POTENTIAL).
CC      SQ SEQUENCE 148 AA; 16518 MW; EEE312496EF513C CRC64;

Query Match      2.3%; Score 7; DB 1; Length 148;
Best Local Similarity 100.0%; Pred.No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 LPLLLLL 21
DB      |||||
        12 LPLLLLL 18

```

Search completed: February 27, 2004, 19:37:56
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 29, 2004, 08:16:48 ; Search time 69 Seconds
(without alignments)
1385.536 Million cell updates/sec

Title: US-10-047-021-86

Perfect score: 303

Sequence: 1 MGSGDLSLLGGRGSLPLLLL.....SGPRLPREARELGRQRRNTG 303

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_25:**

1: sp_archaea:**

2: sp_bacteria:**

3: sp_fungi:**

4: sp_human:**

5: sp_invertebrate:**

6: sp_mammal:**

7: sp_mhc:**

8: sp_organelle:**

9: sp_phage:**

10: sp_plant:**

11: sp_rodent:**

12: sp_virus:**

13: sp_vertebrate:**

14: sp_unclassified:**

15: sp_rvirus:**

16: sp_bacteriaph:**

17: sp_archaeap:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	148	48.8	1007	4 Q8WZ75	Q8WZ75 homo sapien
2	120	39.6	792	4 Q96JY6	Q96JY6 homo sapien
3	69	22.8	702	4 Q8TEG1	Q8TEG1 homo sapien
4	27	8.9	961	11 Q8OW87	Q8OW87 rattus norv
5	27	8.9	1016	11 Q8C310	Q8C310 mus musculus
6	10	3.3	129	11 Q8VB7	Q8VB7 mus musculus
7	10	3.3	424	11 Q8C8W0	Q8C8W0 mus musculus
8	10	3.3	1150	11 Q8BS24	Q8BS24 mus musculus
9	10	3.3	1209	11 P70232	P70232 mus musculus
10	9	3.0	362	9 Q8LTT9	Q8LTT9 bacterioph
11	8	2.6	72	16 Q8YGC5	Q8YGC5 bruceella me
12	8	2.6	123	4 Q86RL5	Q86RL5 homo sapien
13	8	2.6	189	4 Q8WU39	Q8WU39 homo sapien
14	8	2.6	205	6 Q7YRG8	Q7YRG8 cebus albif
15	8	2.6	205	11 Q810Z2	Q810Z2 mus musculus
16	8	2.6	216	11 Q9CST8	Q9CST8 mus musculus

17	8	2.6	227	4 Q9UKJ0	Q9UKJ0 homo sapien
18	8	2.6	233	16 Q9CHY7	Q9CHY7 lactococcus
19	8	2.6	271	4 Q9HBS0	Q9HBS0 homo sapien
20	8	2.6	305	16 Q89U06	Q89U06 bradyrhizob
21	8	2.6	326	10 P93680	P93680 perseia amer
22	8	2.6	353	4 Q86XY3	Q86XY3 homo sapien
23	8	2.6	353	16 Q7UXV9	Q7UXV9 rhodopirell
24	8	2.6	376	2 Q93U15	Q93U15 bradyrhizob
25	8	2.6	420	5 Q8IMW5	Q8IMW5 drosophila
26	8	2.6	431	10 Q9SN38	Q9SN38 arabidopsis
27	8	2.6	436	5 Q9V974	Q9V974 drosophila
28	8	2.6	453	16 Q8UHT2	Q8UHT2 agrobacteri
29	8	2.6	464	11 Q9EPL5	Q9EPL5 mus musculu
30	8	2.6	475	4 Q75255	Q75255 homo sapien
31	8	2.6	526	4 Q8NG09	Q8NG09 homo sapien
32	8	2.6	613	4 Q969P0	Q969P0 homo sapien
33	8	2.6	1501	11 Q9QW00	Q9QW00 rattus sp.
34	8	2.6	1501	11 Q7TTL7	Q7TTL7 mus musculu
35	8	2.6	1502	4 Q9UM81	Q9UM81 homo sapien
36	8	2.6	1626	5 Q9V5X5	Q9V5X5 drosophila
37	8	2.6	1788	13 Q9IAJ0	Q9IAJ0 xenopus lae
38	8	2.6	1863	11 Q64605	Q64605 rattus norv
39	8	2.6	1887	11 Q9QW67	Q9QW67 rattus sp.
40	8	2.6	1894	11 Q64487	Q64487 mus musculu
41	8	2.6	1896	13 Q9IAJ1	Q9IAJ1 xenopus lae
42	8	2.6	1898	4 Q86WS0	Q86WS0 homo sapien
43	8	2.6	1898	11 Q9EQ17	Q9EQ17 mus musculu
44	8	2.6	1898	11 Q64604	Q64604 r protein-t
45	8	2.6	1904	11 Q64699	Q64699 mus musculu

ALIGNMENTS

RESULT 1

Q8WZ75 ID Q8WZ75 PRELIMINARY; PRT; 1007 AA.

AC Q8WZ75;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Magic roundabout.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20530916; PubMed=11076864;
RA Huminiecki L., Bicknell R.;
RT "In silico cloning of novel endothelial-specific genes."
RL Genome Res. 10:1796-1806 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Huminiecki L., Bicknell R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP361473; AAL31867.1; -;
DR Genew; HGNC:17985; ROBO4.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR008957; FN.III-like.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PFC00041; fn3; 2.
DR Pfam; PFC00047; ig1; 2.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IG2; 1.
DR PROSITE; PSS0835; IG_LIKE; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 1007 AA; 107457 MW; E43F246C59BB1415 CRC64;

Query Match 48.8%; Score 148; DB 4; Length 1007;
Best local Similarity 100.0%; Pred. NO. 8.3e-140;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 55 ASGQPPPTIRLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAHQALSTDLGYVTC 114
DB 55 ASGQPPPTIRLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAHQALSTDLGYVTC 114
OY 115 EASNRLGTAVERGARGLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174
DB 115 EASNRLGTAVERGARGLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174
OY 175 GKPLALQPGRHVTSGSLMARAKSDE 202
DB 175 GKPLALQPGRHVTSGSLMARAKSDE 202

RESULT 2
O96JV6
ID Q96JV6 PRELIMINARY; PRT; 792 AA.
AC Q96JV6:
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ14946.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Placenta;
RA Isoqai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Konai F., Hara R., Takeuchi K.,
RA Arica M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK07852; BAB55411.1; -.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS0835; IG_LIKE; 2.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 792 AA; 85419 MW; FC6DC05275B7B234 CRC64;

Query Match 39.6%; Score 120; DB 4; Length 792;
Best Local Similarity 100.0%; Pred. No. 1.le-111;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 55 ASGQPPPTIRLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAHQALSTDLGYVTC 114
DB 55 ASGQPPPTIRLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAHQALSTDLGYVTC 114
OY 115 EASNRLGTAVERGARGLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174
DB 115 EASNRLGTAVERGARGLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174

RESULT 3
O8TEG1
ID O8TEG1 PRELIMINARY; PRT; 702 AA.
AC O8TEG1:
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE FLJ00236 protein (Fragment).
GN FLJ00236.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Spleen;
RA Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;
RT "The nucleotide sequence of a long cDNA clone isolated from human
RT spleen.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK074163; BAB84989.1; -.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin domain.
FT NON_TER 1
SQ SEQUENCE 702 AA; 75340 MW; D668FEE4BCAFDC6 CRC64;

Query Match 22.8%; Score 69; DB 4; Length 702;
Best Local Similarity 100.0%; Pred. No. 2.2e-60;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 134 VLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGLALQPGRHVTSGSLL 193
DB 24 VLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGLALQPGRHVTSGSLL 83
OY 194 MARAKSDE 202
DB 84 MARAKSDE 92

RESULT 4
O80W87
ID O80W87 PRELIMINARY; PRT; 961 AA.
AC O80W87:
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE ROBO4.
GN ROBO4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Roberts K.G., Stewart L.M.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY277635; AAP32918.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003598; IG-like.
DR InterPro; IPR007110; IG_c2.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS0835; IG_LIKE; 2.
DR PROSITE; PS00217; SUGAR_TRANSPORT 2; 1.
SQ SEQUENCE 961 AA; 102579 MW; 1D21E7D4B611899F CRC64;

Query Match 8.9%; Score 27; DB 11; Length 961;

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RT RT "vice deficient for the close homolog of Ll (Chll) display NCAM180
RT mRNA upregulation, abnormal hippocampal mossy fiber connectivity, and
RT altered exploratory behaviour."
RT RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ319655; CAC88131.1; -.
DR EMBL; AJ319656; CAC88131.1; JOINED.
DR EMBL; AJ319657; CAC88131.1; JOINED.
DR InterPro; IPR007110; Ig-like.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 >30 POTENTIAL.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14435 MW; FBFIA5436F9371D2 CRC64;

Query Match 3.3%; Score 10; DB 11; Length 129;
Best Local Similarity 100.0%; Pred.No.0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 ASNRLGTAVS 125
DB 111 ASNRLGTAVS 120
|||||

RESULT 7
Q8C6W0 PRELIMINARY; PRT; 424 AA.
ID Q8C6W0 AC Q8C6W0
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE This close homolog of Ll (Fragment).
GN Chl1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK053039; BAC35247.1; -.
DR MGD; MGI:1098266; Chll.
DR GO; GO:0007411; P-axon guidance; IMP.
DR GO; GO:0007610; P-behavior; IMP.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 4.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS50835; IG_LIKE; 4.
DR NON_TER 424 424
SQ SEQUENCE 424 AA; 47566 MW; C02AC0B8EF5B5805C CRC64;

Query Match 3.3%; Score 10; DB 11; Length 424;
Best Local Similarity 100.0%; Pred.No.0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 ASNRLGTAVS 125
DB 111 ASNRLGTAVS 120
|||||

RESULT 8
Q8BS24 PRELIMINARY; PRT; 1150 AA.
ID Q8BS24 AC Q8BS24

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DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Close homolog of L1.
GN CHL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta, and Vein;
RA MEDLINE=22354683; PubMed=12466851;
RX The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK040765; BAC30699.1; -.
DR MGD; MGI:1098266; Chl1.
DR GO; GO:007411; P:axon guidance; IMP.
DR GO; GO:0007610; P:behavior; IMP.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00041; fn3; 4.
DR SMART; SM00060; FN3; 4.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00409; IG; 5.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS00835; IG_LIKE; 6.
SQ SEQUENCE 1150 AA; 129000 MW; 6C96C082529C7A99 CRC64;
Query Match 3.3%; Score 10; DB 11; Length 1150;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 116 ASNRLGTAVS 125
DB 111 ASNRLGTAVS 120
|||||
RESULT 9
ID P70232 PRELIMINARY; PRT; 1209 AA.
AC P70232;
DT 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE L1-like protein.
GN CHL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Holm J., Hillenbrand R., Steuber V., Bartsch U., Moos M., Luebbert H.,
RA Montag D., Schachner M.;
RT "Structural features of a close homolog of L1 (CHL1) in the mouse: a
RT novel member of the L1 family of neural recognition molecules.";
RL Submitted (DSC-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; X94310; C3A63972.1; -.
DR PIR; T42718; T42718.
DR HSP; P20241; 1CFB.
DR MGD; MGI:1098266; Chl1.
DR GO; GO:007411; P:axon guidance; IMP.
DR GO; GO:0007610; P:behavior; IMP.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN_III-like.

DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00041; fn3; 4.
DR Pfam; PF00047; ig; 6.
DR SMART; SM00060; FN3; 4.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS00835; IG_LIKE; 6.
KW Immunoglobulin domain.
SQ SEQUENCE 1209 AA; 134929 MW; 331F5849AE776226 CRC64;
Query Match 3.3%; Score 10; DB 11; Length 1209;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 116 ASNRLGTAVS 125
DB 111 ASNRLGTAVS 120
|||||
RESULT 10
ID Q8LTT9 PRELIMINARY; PRT; 362 AA.
AC Q8LTT9;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE DNA primase (Fragment).
OS Bacteriophage P4.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OC NCBI_TaxID=10680;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3937;
RA Franza T., Michaud-Soret I., Fiqueret P., Expert D.;
RT "Coupling of iron assimilation and pectinolysis in Erwinia
RT chrysanthemi.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF509493; AAM28906.1; -.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005488; P:binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001993; Mitoch carrier.
DR PROSITE; PS00215; MITOCH_CARRIER; 1.
FT NON_TER 1
FT NON_TER 362
SQ SEQUENCE 362 AA; 38936 MW; CF20E6BDAC873710 CRC64;
Query Match 3.0%; Score 9; DB 9; Length 362;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 82 LLPDGTLL 90
DB 106 LLPDGTLL 114
|||||
RESULT 11
ID Q8YGC5 PRELIMINARY; PRT; 72 AA.
AC Q8YGC5;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Hypothetical membrane associated protein BMEI1234.
GN BMEI1234.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OC NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756688;

RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujar C., Los T.,
 RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
 RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
 RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 RA Haselkorn R., Kyripides N., Overbeek R.,
 RT "The genome sequence of the facultative intracellular pathogen
 RT *Brucella melitensis*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 DR EMBL; AE009562; AAL52415.1; -.
 DR PIR; AD3406;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 72 AA; 8311 MW; D064085089A5AE04 CRC64;
 Query Match 2.6%; Score 8; DB 16; Length 72;
 Best Local Similarity 100.0%; Pred. No. 7.6; 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0;
 Qy 13 GSLPLLLL 20
 Db 44 GSLPLLLL 51
 RESULT 12
 Q96RL5 PRELIMINARY; PRT; 123 AA.
 AC Q96RL5;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Proapoptotic caspase adaptor protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2136986; PubMed=11350957;
 RA Bonfoco E., Li E., Kolbinger F., Cooper N.R.;
 RT "Characterization of a novel proapoptotic caspase-2- and caspase-9-
 RT binding protein.";
 RL J. Biol. Chem. 276:29242-29250(2001).
 DR EMBL; AF38109; AAK84085.1; -.
 SQ SEQUENCE 123 AA; 13066 MW; C21A354CE08A95CB CRC64;
 Query Match 2.6%; Score 8; DB 4; Length 123;
 Best Local Similarity 100.0%; Pred. No. 13; 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0;
 Qy 14 SLPLLLL 21
 Db 4 SLPLLLL 11
 RESULT 13
 Q8WU39 PRELIMINARY; PRT; 189 AA.
 AC Q8WU39;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to RIKEN cDNA 2010001M09 gene.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Tonsil;
 RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC021275; AAK21275.1; -.
 DR InterPro; IPR000886; ER target S.
 DR PROSITE; PS00014; ER_TARGET; 1.

SQ SEQUENCE 189 AA; 20694 MW; C71AED212D3393D3 CRC64;
 Query Match 2.6%; Score 8; DB 4; Length 189;
 Best Local Similarity 100.0%; Pred. No. 19; 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0;
 Qy 14 SLPLLLL 21
 Db 4 SLPLLLL 11
 RESULT 14
 Q7YRG8 PRELIMINARY; PRT; 205 AA.
 AC Q7YRG8;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE LOC122650.
 OS Cebus albifrons (White-fronted capuchin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebus.
 OX NCBI_TaxID=9514;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Devor E.J., Moffat-Wilson K.A.;
 RT "LOC122650 on chromosome 14q11.2 is related to the RNase A superfamily
 RT and contains a unique amino-terminal pre-protein-like domain.";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY330198; AAO01508.1; -.
 SQ SEQUENCE 205 AA; 24294 MW; DBFC3217F7A070D0 CRC64;
 Query Match 2.6%; Score 8; DB 6; Length 205;
 Best Local Similarity 100.0%; Pred. No. 20; 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0;
 Qy 14 SLPLLLL 21
 Db 8 SLPLLLL 15
 RESULT 15
 Q810Z2 PRELIMINARY; PRT; 205 AA.
 AC Q810Z2;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Collagenase-like B (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ;
 RA Brathwaite M., Waeltz P., Nagaraja R.;
 RT "Genomic Sequence Analysis in the Mouse t-complex Region.";
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY211543; AAO37584.1; -.
 DR GO; GO:0005578; C:extracellular matrix; IEA.
 DR GO; GO:0004222; P:metalloendopeptidase activity; IEA.
 DR GO; GO:0008508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR006026; Peptidase M.
 DR InterPro; IPR001818; Pept M10A_M12B.
 DR Pfam; PF00413; Peptidase M10; 1.
 DR Pfam; PF03933; Peptidase M10_N; 1.
 DR PRINTS; PR00138; MATRIXIN.
 DR SMART; SM00235; ZMNC; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 FT NON TER 205 205
 SQ SEQUENCE 205 AA; 23403 MW; DED1E974B8769643 CRC64;

Query Match 2.6%; Score 8; DB 11; Length 205;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 14 SLPLLLLL 21
|||
Db 3 SLPLLLLL 10
|||

Search completed: February 29, 2004, 08:19:08
Job time : 75 secs

29: gb_gss2:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	202	66.7	826	14	CB994099	CB994099 AGENCOURT
2	202	66.7	860	14	CB996189	CB996189 AGENCOURT
3	202	66.7	885	14	CF994298	CF994298 AGENCOURT
4	182	60.1	803	14	CB997292	CB997292 AGENCOURT
5	176	58.1	688	14	CB961818	CB961818 AGENCOURT
6	176	58.1	798	14	CB961529	CB961529 AGENCOURT
7	173	57.1	558	9	AL602474	AL602474 DKFZp6860
8	148	48.8	1019	12	BM921911	BM921911 AGENCOURT
9	148	48.8	3758	11	EC039602	EC039602 Hmo sapi
10	133	43.9	771	14	CB959649	CB959649 AGENCOURT
11	133	43.9	1230	12	BM906521	BM906521 AGENCOURT
12	131	43.2	941	13	BQ90126	BQ90126 AGENCOURT
13	126	41.6	1201	9	AL553360	AL553360 AGENCOURT
14	123	40.6	1028	14	CF994063	CF994063 AGENCOURT
15	110	36.3	797	14	CB961002	CB961002 AGENCOURT
16	109	36.0	502	13	EX474842	EX474842 DKFZp686M
17	107	35.3	610	12	BG745318	BG745318 602723637
18	97	32.0	532	13	EX475138	EX475138 DKFZp6860
19	93	30.7	729	12	BI762862	BI762862 603048384
20	88	29.0	501	13	EX474746	EX474746 DKFZp686B
21	85	28.1	1087	12	BM914311	BM914311 AGENCOURT
22	79	26.1	438	13	EX475177	EX475177 DKFZp686F
23	71	23.4	922	13	EX418142	EX418142 BX418142
24	70	23.1	424	13	EX475172	EX475172 DKFZp686E
25	70	23.1	426	13	EX492967	EX492967 DKFZp781F
26	70	23.1	526	14	CA394658	CA394658 CS54C07.Y
27	63	20.8	344	9	AA577940	AA577940 nl20d01.s
28	63	20.8	450	9	AL039859	AL039859 DKFZp434E
29	51	16.8	1257	14	CB993951	CB993951 AGENCOURT
30	38	12.5	555	12	B1836220	B1836220 603085778
31	35	11.6	570	10	BE233526	BE233526 139756 MA
32	32	10.6	215	13	EX474950	EX474950 DKFZp686I
33	28	9.2	543	29	CE728068	CE728068 tigr-gss-
34	27	8.9	441	13	BY285423	BY285423 BY285423
35	27	8.9	455	10	BB839755	BB839755 BB839755
36	27	8.9	529	13	EX520802	EX520802 BX520802
37	27	8.9	551	9	AI116483	AI116483 ud74C06.Y
38	27	8.9	557	13	BY704924	BY704924 BY704924
39	27	8.9	620	10	BB664621	BB664621 BB664621
40	27	8.9	631	10	BE376779	BE376779 601227331
41	27	8.9	655	14	CF170054	CF170054 B0821H10-
42	27	8.9	662	13	BY727209	BY727209 BY727209
43	27	8.9	3689	11	AK004723	AK004723 Mus muscu
44	27	8.9	3865	11	AK087355	AK087355 Mus muscu
45	25	8.3	264	28	BH257414	BH257414 CH230-243

ALIGNMENTS

RESULT 1
CB994099
LOCUS
DEFINITION AGENCOURT_13642710 NIH MGC 148 Homo sapiens CDNA clone
IMAGE:30331943 5', mRNA sequence.
ACCESSION CB994099
VERSION CB994099
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 826)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 29, 2004, 22:51:24 ; Search time 2913 seconds
(without alignments)
3106.159 Million cell updates/sec

Title: US-10-047-021-86
Perfect score: 303
Sequence: 1 MSGGDSLLGGRSLPLLLL.....SGPLPREARELGGRRNTG 303

Scoring table:
OLIGO Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Delop 6.0 , Delext 7.0

Searched: 27511289 seqs, 14931090276 residues

Word size: 1

Total number of hits satisfying chosen parameters: 55025477

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
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-Q=/cgn2 1/USPTO.spool/US10047021/runat 20022004 154122 4533/app query.fasta_1.455
-DB=EST -QFWT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-NOCALIGN=200 -THR SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFWT=ptc
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-NO MWAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGNAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

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2: em_esthum:*
3: em_estin:*
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6: em_estpl:*
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8: em_hic:*
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11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vit:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*

AUTHORS TITLE JOURNAL COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: NDAM348 row: c column: 24
High quality sequence stop: 637.

FEATURES source

1.826
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30331943"
/tissue_type="pre-eclamptic placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_148"
/note="Organ: placenta; Vector: pBluescriptR; Site 1:
ali-XhoI; Site 2: BamH; Library is oligo-dT primed and
directionally cloned using primer
5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average insert
size 2.3 kb and normalized to ROT 5. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIMH/NHGRI,
National Institutes of Health). Note: this is a NIH_MGC
Library."

ORIGIN

Alignment Scores:
Pred. No.: 3,186-158 Length: 826
Score: 202.00 Matches: 202
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 66.67% Indels: 0
DB: 14 Gaps: 0

US-10-047-021-86 (1-303) x CB994099 (1-826)

Qy	1	MetGlySerGlyAspSerLeuLeuGlyValGlyArgGlySerLeuProLeuLeuLeuLeu 20
Db	38	ATGGGCTCTGGAGGAGACAGCTCTGGGGGGGAGGGGTTCCCTGCTGCTGCTGCTGCTG 97
Qy	21	LeuileMetGlyMetAlaGlnAspSerProGlnleuLeuValHisProGlnAsp 40
Db	98	CTCATCATGGAGGAGTCAGGCTCAGAGTCCCCCGCCAGATCTAGTCCACCCAGGAC 157
Qy	41	GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
Db	158	CAGCTGTTCCAGGGCCCTGGCCCTGCCAGATGAGCTGCCAGCTCAGGCCAGCCACCT 217
Qy	61	ProThrleArgTrpLeuLeuAenGlyGlnProLeuSerMetValProProAspProHis 80
Db	218	CCACCATCCGCTGTTGCTGTAATGGGACGCCCTGAGCATGTGTGCCCCAGACCCACAC 277
Qy	81	HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
Db	278	CACCTCTGCTGATGGAGCCCTTCTGCTACAGCCCTCTGCCGGGAGCATGCCAC 337
Qy	101	AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGlnAlaSerAsnArgLeu 120
Db	338	GATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGCTT 397
Qy	121	GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
Db	398	GGCAGGCGAGTCAGCAGAGGCGCTCGGCTGTCTGTGCTGTCTGCTGCTGCTGCTGCTG 457

Qy	141	IleGlnProArgAspMetValAlaValAlaValGlyGluGlnPheThrleuGluCysGlyPro 160
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Qy	161	ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeu 180
Db	518	CCCTGGGGCCACCCAGAGCCACAGCTCTCATGTGGAAGATGGGAACCCCTGCCCCCTC 577
Qy	181	GlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSer 200
Db	578	CAGCCCGGAAGACACACAGTGTCCGGGGGTCCTGCTGATGGCAAGACGACAGAGAGT 637
Qy	201	AspGlu 202
Db	638	GACGAA 643

CB996189 860 bp mRNA linear EST 01-MAY-2003
AGENCOURT 13622686 NIH_MGC_148 Homo sapiens cDNA clone
IMAGE:30337143 5', mRNA sequence.

CB996189
CB996189.1 GI:30290709
EST.

ORGANISM
Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 860)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Stefan Hansson

cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDAM361 row: 1 column: 16

High quality sequence stop: 578.

Location/Qualifiers

FEATURES

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/lab_host="DH10B Tona"

/clone_lib="NIH_MGC_148"

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ali-XhoI; Site 2: BamH; Library is oligo-dT primed and

directionally cloned using primer

5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average insert

size 2.3 kb and normalized to ROT 5. This is a primary

library enriched for full-length clones and constructed

using the Cap-trapper method (Carninci, in preparation).

Library constructed by M. Brownstein (NIMH/NHGRI,

National Institutes of Health). Note: this is a NIH_MGC

Library."

ORIGIN

Alignment Scores:
Pred. No.: 3,326-158 Length: 860
Score: 202.00 Matches: 202
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 66.67% Indels: 0
DB: 14 Gaps: 0

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: NDAMI069 row: f column: 08
High quality sequence stop: 642.
Location/Qualifiers
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FEATURES
source

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/clone_lib="NIH_MGC_147"
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ORIGIN

Alignment Scores:
Pred. No.: 3,436-158 Length: 885
Score: 202.00 Matches: 202
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 66.67% Indels: 0
DB: 14 Gaps: 0

US-10-047-021-86 (1-303) x CF994298 (1-885)

Qy	1	MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeu 20
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Qy	21	LeuileMetGlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAsp 40
Db	98	CTCATCATGGAGGAGGCTCAGGACTCCCGGCCAGATCTAGTCCACCCCGAGGAC 157
Qy	41	GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
Db	158	CAGCTGTTCCAGGGGCCCTGGCCCTCCAGGATGAGCTGCCGAGCCCTCAGGCGAGCCACCT 217
Qy	61	ProThrIleArgTrrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
Db	218	CCACCATCCGCTGGTGTCTGATGGGACGCCCTGAGCATGTGCCCCCAGACCCACAC 277
Qy	81	HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
Db	278	CACCTCTGCTGATGGGACCCCTTCTGCTGTACAGCCCCCTGCCCGGGGACATGCCAC 337
Qy	101	AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120
Db	338	GATGGCCAGCCCTGTCCACAGACCTGGGTGTCTACATGTGAGGCCAGCACCGGCTT 397
Qy	121	GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
Db	398	GGCAGCGCAGTCAGCAGAGCGCTCGCTGTCTGTGGCTGTCTCCCGGAGGATTTCCAG 457
Qy	141	IleGlnProArgAspMetValAlaValGluGlnPheThrLeuGluCysGlyPro 160
Db	458	ATCCAGCCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGCCG 517
Qy	161	ProTrrpGlyHisProGluProThrValSerTrrpTrrpLysAspGlyLysProLeuAlaLeu 180
Db	518	CCCTGGGGCCACCCAGAGCCACAGTCTCATGTGTGAAAGATGGGAAACCCCTGGCCCTC 577
Qy	181	GlnProGlyArgHisThrValSerGlySerLeuLeuMetAlaArgAlaGluLysSer 200

US-10-047-021-86 (1-303) x CB996189 (1-860)

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Qy	21	LeuileMetGlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAsp 40
Db	98	CTCATCATGGAGGAGGCTCAGGATCTCCCGGCCAGATCTTAGTCCACCCCGAGGAC 157
Qy	41	GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
Db	158	CAGCTGTTCCAGGGGCCCTGGCCCTCCAGGATGAGCTGCCGAGCCTCAGGCGAGCCACCT 217
Qy	61	ProThrIleArgTrrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
Db	218	CCACCATCCGCTGGTGTCTGATGGGACGCCCTGAGCATGTGCCCCCAGACCCACAC 277
Qy	81	HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
Db	278	CACCTCTGCTGATGGGACCCCTTCTGCTGTACAGCCCCCTGCCCGGGGACATGCCAC 337
Qy	101	AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120
Db	338	GATGGCCAGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTT 397
Qy	121	GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
Db	398	GGCAGCGCAGTCACAGAGGCCCTCGGCTGTCTGTGGCTGTCTCCCGGAGGATTTCCAG 457
Qy	141	IleGlnProArgAspMetValAlaValGluGlnPheThrLeuGluCysGlyPro 160
Db	458	ATCCAGCCCTCGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGCCG 517
Qy	161	ProTrrpGlyHisProGluProThrValSerTrrpTrrpLysAspGlyLysProLeuAlaLeu 180
Db	518	CCCTGGGGCCACCCAGAGCCACAGTCTCATGTGTGAAAGATGGGAAACCCCTGGCCCTC 577
Qy	181	GlnProGlyArgHisThrValSerGlySerLeuLeuMetAlaArgAlaGluLysSer 200
Db	578	CAGCCCGAGGACACAGATGTCGGGGGGTCCCTGCTGATGGCAAGCAGCAGAGAGT 637
Qy	201	AspGlu 202
Db	638	GACGAA 643

RESULT 3
CF994298
LOCUS
DEFINITION AGENCOURT_15622355 NIH_MGC_147 Homo sapiens cDNA clone
IMAGE:30706303 5', mRNA sequence.
CF994298
CF994298.1 GI:38510359
EST.
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NCI
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cga@nci.nih.gov

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

```

Db      578 CAGCCCGGAAGGACACACAGTGTCCGGGGGTCCCTGCTGATGGCAAGAGAGAGAGT 637
Qy      201 AspGlu 202
Db      638 GACGAA 643

RESULT 4
LOCUS   CB997292
DEFINITION AGENCOURT 13623935 NIH MGC 148 Homo sapiens cDNA clone
IMAGE:30336795 5', mRNA sequence.
ACCESSION CB997292
VERSION   CB997292.1 GI:30291812
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 803)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM360 row: n column: 04
High quality sequence stop: 535.
Location/Qualifiers
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/clone="IMAGE:30336795"
/tissue_type="pre-eclamptic placenta"
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/clone_lib="NIH_MGC_148"
/note="Organ: placenta; Vector: pBluescriptR; Site 1:
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directionally cloned using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert
size 2.3 kb, and normalized to ROT 5. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIMH/NHGRI).
National Institutes of Health). Note: this is a NIH_MGC
Library."

ALIGNMENT Scores:
Pred. No.: 1.53e-141 Length: 803
Score: 182.00 Matches: 182
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 60.07% Indels: 0
DB: 14 Gaps: 0

US-10-047-021-86 (1-303) x CB997292 (1-803)

Qy      1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20
Db      38 ATGGGCTCTGGAGGAGACAGCTCTCTGGGGGCGAGGGGTTCCCTGCTGCTGCTGCTG 97
Qy      21 LeuileMetGlyGlyMetAlaGlnAspSerProProGlnileLeuValHisProGlnAsp 40
Db      98 CTCATCATGGGAGGACATGGCTCAGGACTCCCGCGCCCGCCAGATCTCTAGTCCACCCCGAGGAC 157

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Qy      41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
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Qy      61 ProThrIleArgTTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
Db      218 CCCACCATCCGCTGTTGCTGAATGGGAGCCCTCGAGCATGGTGGCCCGGAGACCCAC 277
Qy      81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
Db      278 CACCTCTGCTGATGGGACCCTTCTGCTGTACAGCCCCCTGCCCGGGGACATGCCAC 337
Qy      101 AspGlyGlnAlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeu 120
Db      338 GATGGCCAGGCCCTGTCCACAGACCTGGTGTCTACACATGTGAGGCCAGCAACCGGCTT 397
Qy      121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
Db      398 GGACCGCGAGTCCAGCAGAGCGCTCGGTGTCTGTGGTGTCTCTCCGGGAGGATTTCCAG 457
Qy      141 IleGlnProArgAspMetValAlaValGluGlnPheThrLeuGluCysGlyPro 160
Db      458 ATCCAGCCTCGGACATGCTGGTGTGGTGTGAGCAGTTTACTCTGGAATGTGGCGCG 517
Qy      161 ProTrpGlyHisProGluProThrValSerTrpTpyAspGlyLysProLeuAlaLeu 180
Db      518 CCTCGGGGCCACCCAGAGCCACAGTCTCATGTGGAAGATGGGAACCCCTGGCCCTC 577
Qy      181 GlnPro 182
Db      578 CAGCCC 583

RESULT 5
LOCUS   CB961818
DEFINITION AGENCOURT 13665726 NIH MGC 148 Homo sapiens cDNA clone
IMAGE:30349135 5', mRNA sequence.
ACCESSION CB961818
VERSION   CB961818.1 GI:30217935
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 688)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM392 row: p column: 08
High quality sequence stop: 448.
Location/Qualifiers
1..688
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30349135"
/tissue_type="pre-eclamptic placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_148"
/note="Organ: placenta; Vector: pBluescriptR; Site 1:
all-XhoI; Site 2: BamH; Library is oligo-dT primed and
directionally cloned using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert
size 2.3 kb, and normalized to ROT 5. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIMH/NHGRI).
National Institutes of Health). Note: this is a NIH_MGC
Library."

ALIGNMENT Scores:
Pred. No.: 1.53e-141 Length: 803
Score: 182.00 Matches: 182
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 60.07% Indels: 0
DB: 14 Gaps: 0

US-10-047-021-86 (1-303) x CB997292 (1-803)

Qy      1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20
Db      38 ATGGGCTCTGGAGGAGACAGCTCTCTGGGGGCGAGGGGTTCCCTGCTGCTGCTGCTG 97
Qy      21 LeuileMetGlyGlyMetAlaGlnAspSerProProGlnileLeuValHisProGlnAsp 40
Db      98 CTCATCATGGGAGGACATGGCTCAGGACTCCCGCGCCCGCCAGATCTCTAGTCCACCCCGAGGAC 157

```

size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores: 1.22e-136 Length: 688
Pred. No.: 176.00 Matches: 176
Score: 100.00% Conservatives: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 58.09% Gaps: 0
DB: 14

US-10-047-021-86 (1-303) x CB961818 (1-688)

Qy	1	MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeu	20
Db	38	ATGGGCTCTGGAGAGACAGCTCTGGGGGGGAGGGTTCCTGCTGCTGCTGCTG	97
Qy	21	LeuLeuMetGlyGlyMetAlaGlnAspSerProGlnLeuValHisProGlnAsp	40
Db	98	CTATCATGGGAGCATGGCTCAGGACTCCCGCCCGCAGATCTTAGTCCACCCCGAG	157
Qy	41	GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnPro	60
Db	158	CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGTGGCCGAGCCTCAGCCACCT	217
Qy	61	ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspPro	80
Db	218	CCACCATCCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	277
Qy	81	HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis	100
Db	278	CACCTCTGCTGATGGAGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	337
Qy	101	AspGlyGlnAlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeu	120
Db	338	GATGGCCAGCCCTGTCACAGACCTGGGTGCTTACACATGTCAGGCGCAGCAAC	397
Qy	121	GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPhe	140
Db	398	GGCAGCGGAGTACAGAGCGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	457
Qy	141	IleGlnProArgAspMetValAlaValGlyGlnGlnPheThrLeuGluCysGlyPro	160
Db	458	ATCCAGCCTCGGACATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	517
Qy	161	ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLys	176
Db	518	CCCTGGGGCCACCCAGAGCCACAGTCTCATGGTGGAAAGATGGGAAA	565

RESULT 6
CB961529
LOCUS
DEFINITION
AGENCOURT_13893367 NIH_MGC_148 Homo sapiens cDNA clone
IMAGE:30348011 5', mRNA sequence.

ACCESSION
VERSION
CB961529.1 GI:30217646
KEYWORDS
EST.
SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 798)
NIH-MGC <http://mgi.nci.nih.gov/>.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: c9pbbs-remail.nih.gov
Tissue Procurement: Dr. Stefan Hansson

cdNA Library Preparation: Michael J. Brownstein (NHGRI) with help and advice from Piero Carninci (RIKEN)
cdNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: NDAM390 row: a column: 12
High quality sequence stop: 565.

FEATURES
source

Location/Qualifiers
1..798
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30348011"
/tissue_type="pre-eclamptic placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_148"
/note="Organ: placenta; Vector: pBluescriptR; Site 1:
all-XhoI; Site 2: BamH; Library is oligo-dT primed and
directionally cloned using primer
5'-TTTTTTTTTTTNN-3', size-selected for average insert
size 2.3 kb and normalized to ROT 5. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIMH/NHGRI,
National Institutes of Health). Note: this is a NIH_MGC
Library."

ORIGIN

Alignment Scores: 1.55e-136 Length: 798
Pred. No.: 176.00 Matches: 176
Score: 100.00% Conservatives: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 58.09% Gaps: 0
DB: 14

US-10-047-021-86 (1-303) x CB961529 (1-798)

Qy	1	MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeu	20
Db	38	ATGGGCTCTGGAGAGACAGCTCTGGGGGGGAGGGTTCCTGCTGCTGCTGCTG	97
Qy	21	LeuLeuMetGlyGlyMetAlaGlnAspSerProGlnLeuValHisProGlnAsp	40
Db	98	CTATCATGGGAGCATGGCTCAGGACTCCCGCCCGCAGATCTTAGTCCACCCCGAG	157
Qy	41	GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnPro	60
Db	158	CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGTGGCCGAGCCTCAGCCACCT	217
Qy	61	ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspPro	80
Db	218	CCACCATCCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	277
Qy	81	HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis	100
Db	278	CACCTCTGCTGATGGAGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	337
Qy	101	AspGlyGlnAlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeu	120
Db	338	GATGGCCAGCCCTGTCACAGACCTGGCTGCTGCTGCTGCTGCTGCTGCTGCT	397
Qy	121	GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPhe	140
Db	398	GGCAGCGGAGTACAGAGCGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	457
Qy	141	IleGlnProArgAspMetValAlaValGlyGlnGlnPheThrLeuGluCysGlyPro	160
Db	458	ATCCAGCCTCGGACATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	517
Qy	161	ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLys	176

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Db      518 CCCTGGGCGCCAGAGCCACAGTCTCATGTTGGAAAGATGGAAA 565
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RESULT 7
LOCUS   AL602474
DEFINITION DKEZp68601413 r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
ACCESSION DKEZp68601413 5', mRNA sequence.
VERSION   AL602474
KEYWORDS  AL602474.1 GI:15165980
SOURCE    EST.
ORGANISM  Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 558)
AUTHORS   Ansgorge,W., Wirkner,U., Mewes,W., Weil,B. and Wiemann,S.
TITLE     EST (Ansgorge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann,S.)
JOURNAL   Unpublished (1999)
COMMENT   Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone (DKEZp68601413) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
source
1..558
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKEZp68601413"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hlcc3)"
/note="vector: pRipEx2; Site 1: SfIIA; Site 2: SfiIB;
cDNA-collection"
ORIGIN
Alignment Scores:
Pred. No.: 3.34e-134 Length: 558
Score: 173.00 Matches: 173
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.10% Indels: 0
DB: 9 Gaps: 0
US-10-047-021-86 (1-303) x AL602474 (1-558)
QY 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20
Db 40 ATGGGCTCTGGAGGAGACAGCTCTCTGGGGGGCAGGGGTTCCCTGCTGCTGCTGCTG 99
QY 21 LeuLeuMetGlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAsp 40
Db 100 CTCATCATGGAGGAGCATGGCTCAGGACTCCCGCCCGCCAGACTCTAGTTCACCCCGAGGAC 159
QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
Db 160 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGATGAGCTGCCGAGCTCAGGCCAGCACCT 219
QY 61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
Db 220 CCACCATCCGCTGTTGCTGAATGGCAGCCCTCAGCATGTTGTCGCCCGCCAGACCCACAC 279
QY 81 HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
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Db      280 CACCTCCTGCTGATGGGACCCTTCTGCTGTCTACAGCCCTGTCGGGGGACATGCCAC 339
QY 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeu 120
Db 340 GATGGCCAGCCCTGTCACAGACCTGGGTGCTACACATGTGAGCCAGAACCGGTT 399
QY 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
Db 400 GCACGGCAGTCTCAGCAGAGCGCTCGGCTGCTGTGGTGTCTCTCCGGGAGGATTTCCAG 459
QY 141 IleGlnProArgAspMetValAlaValGlnGlnPheThrLeuGluCysGlyPro 160
Db 460 ATCCAGCTCTGGGACATGCTGCTGTGGGTGAGCAGTCTTACTCTGGAATGTGGCGCG 519
QY 161 ProTTPGlyHisProGluProThrValSerTrpTrpLys 173
Db 520 CCCTGGGGCCACCCAGAGCCACACTCTCATGTTGGAAA 558
RESULT 8
LOCUS   BM921911
DEFINITION AGENCOURT 6706908 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5753515
5', mRNA sequence.
ACCESSION BM921911
VERSION   BM921911.1 GI:19372290
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1019)
AUTHORS   NIH-MGC http://mgi.cni.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12789 row: g column: 20
High quality sequence stop: 697.
FEATURES
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1..1019
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5753515"
/lab_host="DH10B"
/clone_lib="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
cligo-AT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.: 4.79e-113 Length: 1019
Score: 148.00 Matches: 211
Percent Similarity: 99.06% Conservative: 0
Best Local Similarity: 99.06% Mismatches: 1
Query Match: 48.84% Indels: 2
DB: 12 Gaps: 0

```

contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettman, Anuradha Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 84 Row: i Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Genescan gene prediction
This clone has the following problem: frame shifted.

FEATURES
Location/Qualifiers
source
1..3758
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5590503"
/tissue_type="Ovary, pooled from 3 adults"
/clone_lib="NIH MGC_125"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN
Alignment Scores:
Pred. No.: 2,018-112 Length: 3758
Score: 148.00 Matches: 264
Percent Similarity: 98.51% Conservative: 0
Best Local Similarity: 98.51% Mismatches: 2
Query Match: 48.84% Indels: 4
DB: 11 Gaps: 0

US-10-047-021-86 (1-303) x BC039602 (1-3758)

QY 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20
Db 29 AIGGGCTCTGGAGAGACAGCCCTCTGGGGGACAGGGTTCCTGCTCTGCTCTG 88
QY 21 LeuLeuMetGlyGlyMetAlaGlnAspSerProGlnGlnLeuValHisProGlnAsp 40
Db 89 CTCATCATGGGAGGATGGCTCAGGACTCCCGCCAGATCCTAGTCACCCCGAGAC 148
QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnPro 60
Db 149 CAGCTGTTCAGGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCACCCACC 207
QY 60 OProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHi 80
Db 208 TCCACCATCCCTGGTTCGTAATGGGACGCCCTGAGCATGTGTCCTCCAGACCCACA 267
QY 80 stHisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHi 100
Db 268 CCACCTCTCTGCTGTGGACCCCTTCGCTGTACAGACCCCTGCGGGGACATGCCCA 327
QY 100 sAspGlyGlnAlaLeuSerThrAspLeuGlyValTyThrCysGluAlaSerAsnArg 120
Db 328 CGATGGCCAGGCCCTGTCCAGACCTGGGTCTTACACATGTGAGGCCAGCAACCGCT 387
QY 120 uGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheG 140
Db 388 TGGCAGCGCAGT-CAGCAGAGGCCCTCGGTCTCTGTGGCTGTCTCCCGGGAGATTCCA 447
QY 140 nileGlnProArgAspMetValAlaValValGlyGlnGlnPheThrLeuGluCysGlyPr 160
Db 448 GATCCAGCTCCGGACATGGTGGCTGTGGTGGGTGAGCAGATTACTCTGGAAATGGGCC 507
QY 160 OProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAla 180
Db 508 GCCCTGGGGCCACCAGAGCCACAGTCTCATGTGTGAAAGATGGAAACCCCTGGCCCT 567
QY 180 uGlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGlyLys 200
Db 568 CCAGCCCGGAGGACACAGATGTCCGGGGGGTCCCTGCTGTGTGAGCAGAGAGAG 627

US-10-047-021-86 (1-303) x BM921911 (1-1019)

QY 55 AlaSerGlyGlnProProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMet 74
Db 76 GCCTCAGCCAGCACCTCCACCATCCGCTGGTGTGTAATGGGACGCCCTGAGCATG 135
QY 75 ValProProAspProHisHisLeuLeuProAspGlyThrLeuLeuLeuGlnProPro 94
Db 136 GTGCCCCCAGACCCACACCTCTCTGCTGTGGACCTTCTGCTGTACAGCCCTT 195
QY 95 AlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThrAspLeuGlyValTyThrCys 114
Db 196 GCCCGGGACATGCCACGATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTACATGT 255
QY 115 GluAlaSerAsnArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaVal 134
Db 256 GAGCCAGCAACCGCTGTGCACGGCAGTCAGCAGAGGCCCTCGGCTGTCTGGCTGTC 315
QY 135 LeuArgGluAspPheGlnGlnProArgAspMetValAlaValValGlyGlnGlnPhe 154
Db 316 CTCGGGAGGATTTCCAGATCCAGCTCCGGACATGGTGGCTGTGGTGGTGAAGCAGTT 375
QY 155 ThrLeuGluCysGlyProProTrpGlyHisProGluProThrValSerTrpTrpLysAsp 174
Db 376 ACTCTGAATGTGGCGCCCTGGGGCCACCCAGAGCCACAGTCTCATGTGGAAGAT 435
QY 175 GlyLysProLeuAlaLeuGlnProGlyArgHisThrValSerGlyGlySerLeuLeuMet 194
Db 436 GGGAAACCCCTGGCCCTCCAGCCGGAAGACACAGTGTCCGGGGTCCCTGCTGATG 495
QY 195 AlaArgAlaGlyLysSerAspGlu***-ThrTyMetCysValAlaThrAsnSerAlaG 214
Db 496 GCAAGACAGAGAAGAGTACGAGAGG-GACCTACATGTGTGTGGCCACCAACAGCGCAGG 554
QY 214 YHisArgGluSerArgAlaAlaArgValSerIleGlnGlnProGlnAspTyThrGluPr 234
Db 555 ACATAGGAGAGCGCGCAGCCGGGTTTCATCCAGAGGCCCCAGGACTACACGAGGCC 614
QY 234 oValGluLeuLeuAlaValArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspPr 254
Db 615 TGTGAGCTTCTGGCTGTGGATTCAGCTGGAATGTGACACTGTGTGACCCGGATCC 674
QY 254 oAlaGluGlyProLysProArgProAlaValTrpLeu 266
Db 675 TGCAGAGGGCCCCAAGCCTAGACCGCGGTGTGGCTC 711

RESULT 9
BC039602
LOCUS
DEFINITION Homo sapiens, Similar to roundabout homolog 4, magic roundabout.
(Drosophila), clone IMAGE:5590503, mRNA.
ACCESSION BC039602
VERSION BC039602.1 GI:24660430
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3758)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (01-NOV-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgap@remail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbiology.org>

```

QY 200 rAspGlu***-ThrTyMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgA 220
DB 628 TGACGAAGG-GACCTACATGTGTGTGGCCACCAACAGCGGAGGACATAGGAGCGCG 686

QY 220 laAlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuAlaVal 240
DB 687 CAGCCCGGGTTTCATCCAGAGGCCAGGACTACAGGAGCCCTGTGGAGCTTCTGGCTG 746

QY 240 alaGileGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysP 260
DB 747 TGCGAATTCAGCTGGAAATGTGACACTGCTGTAACCCGGATCTCTGACAGGGGCCCAAGC 806

QY 260 rCArgProAlaValTrieu 266
DB 807 CTAGACCGGGCGGTGGCTC 826

RESULT 10
LOCUS CB959649 771 bp mRNA linear EST 29-APR-2003
DEFINITION AGENCOURT_13893577 NIH_MGC_147 Homo sapiens cDNA clone
IMAGE:30344820 5', mRNA sequence.
ACCESSION CB959649
VERSION CB959649.1 GI:30215765
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 771)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGR) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM381 row: 1 column: 13
High quality sequence stop: 628.
FEATURES
source
1..771
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30344820"
/tissue_type="Human Placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_147"
/note="Organ: Placenta; Vector: pBluescriptR; Site: 1:
all-XhoI; Site 2: BamH; Oligo-dr primed using primer
5'-TTTTTTTTTTTTTNN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGR). National Institutes of Health. Note: This is
a NIH_MGC library."

ORIGIN
Alignment Scores:
Pred. No.: 1..17e-100 Length: 771
Score: 133.00 Matches: 186
Percent Similarity: 98.94% Conservative: 0
Best Local Similarity: 98.94% Mismatches: 1
Query Match: 43.89% Indels: 2
DB: 14 Gaps: 0

US-10-047-021-86 (1-303) x CB959649 (1-771)

```

```

QY 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeu 20
DB 66 ATGGGCTCTGAGGAGACAGCCTCTCTGGGGGGCAGGGGTTCCCTGCTCTGCTGCTCTG 125

QY 21 leuLleMetGlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAsp 40
DB 126 CTCATCATGGGAGGAGCATGGCTCAGACTCCCGCCGAGATCCTAGTCCACCCAGGAC 185

QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProPr 60
DB 186 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGTCCCA-AGCCTCAGGCCAGCCACC 244

QY 60 oProThrIleArgTyrLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHi 80
DB 245 TCCACCACTCCGCTGGTTGCTGAATGGGACGCCCTGAGCATGGTGGCCCGGAGACCCACA 304

QY 80 sHisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHi 100
DB 305 CCACCTCTCTGCTGATGGGACCCCTTCTGCTGTACAGCCCTTCCCGGGGACATGCCCA 364

QY 100 sAspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLe 120
DB 365 CGATGGCCAGGCCCTGTCCACAGACCTGGGTGCTTACACATGTGAGGCGACAGCCGGCT 424

QY 120 uGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheG 140
DB 425 TGGCAGGCGATCAGACAGAGCGCTCGGCTGTCTGTGGTCTCTCTCCGGGAGGATTTCCA 484

QY 140 nileGlnProArgAspMetValAlaValAlaValGlyGlnGlnPheThrLeuGluCysGlyPr 160
DB 485 GATCCAGCCTCGGACATGGTGGCTGTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 544

QY 160 oProThrGlyHisProGluProThrValSerTyrTrpLysAspGlyLysProLeuAlaLe 180
DB 545 GCCCTGGGGGCCACCCAGAGCCACAGTCTCATGGTGGAAAGATGGGAACCCCTGGGCC 604

QY 180 uGlnProGlyArgHisThrVal 187
DB 605 CCAGCCCCGGAAGGCACACAGTG 626

RESULT 11
LOCUS BM906521 1230 bp mRNA linear EST 12-MAR-2002
DEFINITION AGENCOURT_6620212 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5590503
5', mRNA sequence.
ACCESSION BM906521
VERSION BM906521.1 GI:19356900
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1230)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12364 row: 0 column: 16
High quality sequence stop: 535.
FEATURES
source
1..1230
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

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/clone="IMAGE:5590503"
/lab_host="DH10B"
/clone_lib="NIH_MGC_125"
/notes="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
Site1: Scov (destroyed); Site2: NotI; RNA source pool
of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."

```

ORIGIN

Alignment Scores:
 Pred. No.: 1.96e-100 Length: 1230
 Score: 133.00 Matches: 186
 Percent Similarity: 98.94% Conservative: 0
 Best Local Similarity: 98.94% Mismatches: 1
 Query Match: 43.89% Indels: 2
 DB: 12 Gaps: 0

US-10-047-021-86 (1-303) x BM906521 (1-1230)

QY	1	MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeu 20
DB	35	ATGGGCTCTGAGGAGACACCTCTGGGGGAGAGGGTTCCTGCTCTGCTGCTCTG 94
QY	21	LeuLeuMetGlyGlyMetAlaGlnAspSerProProGlnLeuValHisProGlnAsp 40
DB	95	CTCATCTGGAGGAGGATGGCTAGGACTCCCGCCCGAGATCTAGTCCACCCCGAGGAC 154
QY	41	GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProPr 60
DB	155	CAGCTGTTCAGGGCCCTGGCCCTGCCAGGATGAGTGCCA-AGCCTCAGGCGAGCCACC 213
QY	60	oProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHi 80
DB	214	TCCACCATCGCTGGTGTGATGGGAGCGCCCTCAGCATGGTGTGCCCCAGACCCACA 273
QY	80	sHisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHi 100
DB	274	CCACCTCTGCTGATGGACCTCTGCTGCTACAGCCCTGCTGCTGCTGCTGCTGCTG 333
QY	100	sAspGlyGlnAlaLeuSerThrAspLeuGlyValThrCysGlnAlaSerAsnArgLe 120
DB	334	CGATGGCCAGGCCCTGTCACAGACCTGGGTGCTACATGTGAGCCAGCACCGGCT 393
QY	120	uGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGl 140
DB	394	TGGCAGGCGCATCAGCAGGCGCTGGCTGTCTGTGCTGCTGCTGCTGCTGCTGCTG 453
QY	140	nIleGlnProArgAspMetValAlaValValGlyGlnPheThrLeuGluCysGlyPr 160
DB	454	GATCCAGCTCGGAGACATGGTGGCTGTGGTGAGCAGTTTACTCTGGAATGTGGGCC 513
QY	160	oProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLe 180
DB	514	GCCTGGGGGCCACCCAGAGCCACAGTCTCATGTGGGAAGATGGAAACCCCTGGCCCT 573
QY	180	uGlnProGlyArgHisThrVal 187
DB	574	CCAGCCCGAAGGCACACAGTG 595

RESULT 12
 BQ890126
 LOCUS BQ890126 941 bp mRNA linear EST 16-AUG-2002
 DEFINITION AGENCOURT 7982449 Lupski_dorsal_root ganglion Homo sapiens cDNA
 clone IMAGE:6186214 5', mRNA sequence.
 ACCESSION BQ890126
 VERSION BQ890126.1 GI:22282140
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 941)
 NIH-MGC http://mhc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-remail.nih.gov

Tissue Procurement: Dr. James R. Lupski
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: LHAM13578 row: d column: 23
 High quality sequence start: 6
 High quality sequence stop: 612.

FEATURES

source

1..941
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6186214"
 /sex="male"
 /tissue_type="dorsal root ganglia"
 /dev_stage="adult, 36 yr"
 /lab_host="DH10B"
 /clone_lib="Lupski dorsal root ganglion"
 /note="Vector: pCMV-SPORT6 (Life Technologies); Site 1:
 NotI; Site 2: SalI; cDNA made by oligo-dT priming.
 Directionally cloned using the following adaptors:
 5'-TCGACCCAGCGTCCG-3' and
 5'-GACTAGTCTAGATCGAGCGCGCCT(15)-3'. Size selected >
 1 kb for average insert length 1.7 kb. This is a primary
 library, non-amplified. Library constructed by Life
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
 College of Medicine) and is available through Life
 Technologies."

ORIGIN

Alignment Scores:
 Pred. No.: 6.82e-99 Length: 941
 Score: 131.00 Matches: 184
 Percent Similarity: 98.92% Conservative: 0
 Best Local Similarity: 98.92% Mismatches: 1
 Query Match: 43.23% Indels: 2
 DB: 13 Gaps: 0

US-10-047-021-86 (1-303) x BQ890126 (1-941)

QY	1	MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20
DB	53	ATGGGCTCTGAGGAGACACCTCTGGGGGAGAGGGTTCCTGCTCTGCTGCTCTG 112
QY	21	LeuLeuMetGlyGlyMetAlaGlnAspSerProGlnLeuValHisProGlnAsp 40
DB	113	CTCATCTGGAGGAGGATGGCTAGGACTCCCGCCCGAGATCTAGTCCACCCCGAGGAC 172
QY	41	GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProPr 60
DB	173	CAGCTGTTCAGGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 231
QY	60	oProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHi 80
DB	232	TCCACCATCGCTGGTGTGCTGAATGGGAGCCCTGAGCATGGTGTGCTGCTGCTG 291
QY	80	sHisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHi 100
DB	292	CCACCTCTGCTGATGGGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 351
QY	100	sAspGlyGlnAlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLe 120


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Db      352 CGATGCCAGGCCCTGTCCACAGACTGGTGTCTACACATGTGAGGCACGACCGGCT 411
QY      120 uGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheG1 140
Db      412 TGGCAGCGGAGTCAGCAGAGGCGCTCGGTGTCTGTGGCTGTCTCCGCGGAGGATTCCCA 471
QY      140 nileGlnProArgAspMetValAlaValValGlyClnGlnPheThrLeuGluCysGlyPr 160
Db      472 GATCCAGCCTCGGACATGGTGGCTGTGTGGTGGAGCAGTTTACTCTGGAATGTGGGCC 531
QY      160 oProTIPGlyHisProGluProThrValSerTIPTrpLysAspGlyLysProLeuAlaLe 180
Db      532 GCCTGGGGCCACCCAGAGGCCACAGTCTCATGTGTGGAAAGATGGGAACCCCTGGCCCT 591
QY      180 uGlnProGlyArgHis 185
Db      592 CCAGCCCGAAGGCAC 607

RESULT 13
AL553360
LOCUS
DEFINITION
AL553360 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1075YP13 5-PRIME, mRNA sequence.
ACCESSION
AL553360
VERSION
AL553360.2 GI:31275174
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL
On Feb 15, 2001 this sequence version replaced gi:12893123.
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6206.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D1075CH07QPI&cluster=6206.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0D1075CH07QPI.
FEATURES
Location/Qualifiers
source
1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1075YP13"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with NotI and cloned into the NotI and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Alignment Scores:
Pred. No.: 1.33e-94 Length: 1201
Score: 126.00 Matches: 179
Percent Similarity: 98.90% Conservative: 0
Best Local Similarity: 98.90% Mismatches: 1
Query Match: 41.58% Indels: 2
DB: 9 Gaps: 0

US-10-047-021-86 (1-303) x AL553360 (1-1201)
QY 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerProLeuLeuLeu 20

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Db      81 ATGGGCTCTGGAGGACACAGCCCTCTGGGGGGCAGGGGTTCCTCTGCTGCTCTG 140
QY      21 LeuileMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp 40
Db      141 CTCATCATGGAGGCATGGCTCAGGACTCCCGCCGCCAGATCTTAGTCCACCCAGGAC 200
QY      41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProPr 60
Db      201 CAGCTCTTCCAGGGCCCTGGCCCTGCGCAGGATGAGTGCCA-AGCCTCAGGCGCAGCCACC 259
QY      60 oProThrIleArgTIPLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHi 80
Db      260 TCCACACATCCGCTGGTGTCTGAATGGGCGAGCCCTTGACATGGTGGCCCCCAGACCA 319
QY      80 sHisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHi 100
Db      320 CCACCTCTCTGCTGATGGGACCCCTTCTGTGCTACAGCCCCCTGCCCGGGGACATGCCA 379
QY      100 sAspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLe 120
Db      380 CGATGGCCAGGGCCCTGTCCACAGACTGGGTGTCTACACATGTGAGGCGCAGCAACGGCT 439
QY      120 uGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheG1 140
Db      440 TGGCAGCGGAGTCAGCAGAGGCGCTCGGTGTCTGTGGCTGTCTCCGCGGAGGATTCCCA 499
QY      140 nileGlnProArgAspMetValAlaValValGlyClnGlnPheThrLeuGluCysGlyPr 160
Db      500 GATCCAGCCTCGGACATGGTGGCTGTGTGGTGGAGCAGTTTACTCTGGAATGTGGGCC 559
QY      160 oProTIPGlyHisProGluProThrValSerTIPTrpLysAspGlyLysProLeuAlaLe 180
Db      560 GCCTGGGGCCACCCAGAGGCCACAGTCTCATGTGTGGAAAGATGGGAACCCCTGGCCCT 619
QY      180 u 180
Db      620 C 620

CF994063 1028 bp mRNA linear EST 25-NOV-2003
AGENCOURT 15622361 NIH_MGC_147 Homo sapiens cDNA clone
IMAGE:30519942 5', mRNA sequence.
CF994063
VERSION
CF994063.1 GI:38510123
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. (bases 1 to 1028)
NIH-MGC http://mgi.nci.nih.gov/.
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
UNPUBLISHED (1999)
CONTACT: DANIELA S. GERHARD, Ph.D.
OFFICE OF CANCER GENOMICS
NATIONAL CANCER INSTITUTE / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LML at:
http://image.llnl.gov
Plate: NDAM592 row: e column: 07
High quality sequence stop: 411.
Location/Qualifiers
1..1028
/organism="Homo sapiens"
FEATURES
source

```


Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: NDAM379 row: a column: 15
High quality sequence stop: 475.
Location/Qualifiers
1. 797
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30343790"
/tissue_type="Human Placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC 147"
/note="Organ: placenta; Vector: pBluescriptR; Site: 1:
all-XhoI; Site 2: BamH; Oligo-dT primed using primer
5'-TTTTTTTTTTTNN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: This is
a NIH_MGC library."

ORIGIN

Alignment Scores:

Pred. No.:	1.93e-81	Length:	797
Score:	110.00	Matches:	152
Percent Similarity:	98.70%	Conservative:	0
Best Local Similarity:	98.70%	Mismatches:	1
Query Match:	36.30%	Indels:	2
DB:	14	Gaps:	0

US-10-047-021-86 (1-303) x CB961002 (1-797)

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30519942"
/tissue_type="Human Placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC 147"
/note="Organ: placenta; Vector: pBluescriptR; Site: 1:
all-XhoI; Site 2: BamH; Oligo-dT primed using primer
5'-TTTTTTTTTTTNN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: This is
a NIH_MGC library."

ORIGIN

Alignment Scores:

Pred. No.:	3.58e-92	Length:	1028
Score:	123.00	Matches:	123
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	40.59%	Indels:	0
DB:	14	Gaps:	0

US-10-047-021-86 (1-303) x CF994063 (1-1028)

Qy 1 MetGlySerGlyCysArgSerLeuLeuGlyCysArgGlySerLeuProLeuLeuLeu 20
Db ATGGGCTCTGGAGGAGACAGCTCTGGGGGCGAGGGGTTCCCTGCCTCTGCTCTCTG 97

Qy 21 LeuLeuMetGlyCysMetAlaGlnAspSerProGlnLeuValHisProGlnAsp 40
Db 98 CTCATCATGGAGGATGGCTCAGAGATCCCGCCGCCAGATCTTATGTCACCCCGAGAC 157

Qy 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
Db 158 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGATGAGCTGCCAGCTCAGGCCACCCACCT 217

Qy 61 ProThrLeuArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
Db 218 CCCACCATCCCTGGTGTGTAATGGGCGAGCCCTGAGCATGGTGCCCGGAGACCCACAC 277

Qy 81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
Db 278 CACTCTCTGCTGATGGACCTCTCTGTCTAGACCCCTGCGCGGGACATGCCAC 337

Qy 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120
Db 338 GATGCCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGCTT 397

Qy 121 GlyThrAla 123
Db 398 GGCACGGCA 406

RESULT 15
CB961002
LOCUS
DEFINITION
AGENCOURT 13761727 NIH_MGC 147 Homo sapiens cDNA clone
IMAGE:30343790 5', mRNA sequence.
CB961002
VERSION
CB961002.1 GI:30217119
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 797)
NIH-MGC <http://mgc.mci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Thu Mar 4 06:51:02 2004

us-10-047-021-86.rst

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Search completed: March 1, 2004, 09:17:43
Job time : 2926 secs